

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 31, 2002, 12:18:05 ; Search time 12.94 Seconds
(without alignments)
15.101 Million cell updates/sec

Title: US-09-516-728-1

Perfect score: 8

Sequence: 1 OSRDTEVL 8

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	100.0	1337	3	US-08-854-585-2
2	8	100.0	1337	5	PCT-US95-05512-2
3	5	62.5	16	2	US-08-318-837-28
4	5	62.5	20	2	US-08-318-837-4
5	5	62.5	122	1	US-08-326-117B-14
6	5	62.5	122	1	US-08-982-129-14
7	5	62.5	178	1	US-08-928-443-1
8	5	62.5	178	3	US-09-129-055-1
9	5	62.5	311	2	US-08-318-837-7
10	5	62.5	311	2	US-08-318-837-9
11	5	62.5	313	1	US-08-078-683A-4
12	5	62.5	357	1	US-08-356-405-2
13	5	62.5	371	4	US-08-806-263-2
14	5	62.5	380	4	US-08-969-815-4
15	5	62.5	380	4	US-09-120-025-4
16	5	62.5	419	1	US-08-385-186-2
17	5	62.5	419	1	US-08-385-186-4
18	5	62.5	465	4	US-09-150-440-1
19	5	62.5	663	1	US-07-912-015-2
20	5	62.5	740	1	US-08-309-512-10
21	5	62.5	740	5	PCT-US92-08756A-10
22	5	62.5	765	1	US-08-309-512-5
23	5	62.5	765	5	PCT-US92-08756A-5
24	5	62.5	1019	1	US-08-271-364A-7
25	5	62.5	1019	2	US-08-222-715B-26
26	5	62.5	1100	1	US-08-357-598-11
27	5	62.5	1100	2	US-09-003-289-11

28	5	62.5	1100	5	PCT-US95-16435-11	Sequence 11, Appl
29	5	62.5	1455	2	US-08-726-012B-2	Sequence 2, Appl
30	5	62.5	1462	3	US-07-792-600-31	Sequence 31, Appl
31	5	62.5	1462	3	US-09-157-021-31	Sequence 31, Appl
32	5	62.5	1462	3	US-09-156-842-31	Sequence 31, Appl
33	5	62.5	1528	3	US-08-326-117B-2	Sequence 2, Appl
34	5	62.5	1528	3	US-08-982-129-2	Sequence 2, Appl
35	5	62.5	1792	2	US-08-962-284-4	Sequence 4, Appl
36	5	62.5	2409	6	5180808-2	Patent No. 5180808
37	5	62.5	3033	1	US-07-925-695-8	Sequence 8, Appl
38	5	62.5	3033	1	US-07-925-695-9	Sequence 9, Appl
39	5	62.5	3079	5	PCT-US94-00198-4	Sequence 4, Appl
40	4	50.0	6	4	US-09-187-859-3511	Sequence 3511, Ap
41	4	50.0	7	4	US-09-187-859-3514	Sequence 3514, Ap
42	4	50.0	7	4	US-09-187-859-3526	Sequence 3526, Ap
43	4	50.0	8	2	US-08-726-306A-181	Sequence 181, App
44	4	50.0	8	3	US-09-188-579-26	Sequence 26, Appl
45	4	50.0	8	3	US-09-188-579-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1

US-08-854-585-2
; Sequence 2, Application US/08854585

Patent No. 6114140
; GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K. and stman, Arne
; TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase

NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, Suite 6300

CITY: Chicago
; STATE: Illinois

COUNTRY: United States of America
; ZIP: 60606

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/854,585
; FILING DATE:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,940

FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael P.
; REGISTRATION NUMBER: 25,447

REFERENCE/DOCKET NUMBER: 27866/31954
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

LENGTH: 1337 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-854-585-2

Query Match 100.0%; Score 8; DB 3; Length 1337;

Best Local Similarity 100.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0;

QY 1 OSRDTEVL 8
Db 324 OSRDTEVL 331

RESULT 2
PCT-US95-05512-2
Sequence 2, Application PC/TUS9505512
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and Stman, Arne
TITLE OF INVENTION: Densitly Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05512-2

Query Match 100.0%; Score 8; DB 5; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSRDTEVL 8
DB 324 QSRDTEVL 331

RESULT 3
US-08-318-837-28
Sequence 28, Application US/08318837
Patent No. 5981277
GENERAL INFORMATION:
APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEVERSMYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY C
TITLE OF INVENTION: IMMUNOLOGY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,401,231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Mouse, human
CELL LINE: PUS-1.8, THP-1
US-08-318-837-28

Query Match 62.5%; Score 5; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DTEVL 8
DB 10 DTEVL 14

RESULT 4
US-08-318-837-4
Sequence 4, Application US/08318837
Patent No. 5981277
GENERAL INFORMATION:
APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEVERSMYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAP
TITLE OF INVENTION: IMMUNOLOGY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,401,231.3
FILING DATE: 30-APR-1992

ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-837-4

Query Match 62.5%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
DB 8 DTEVL 12

RESULT 5
US-08-326-117B-14
Sequence 14, Application US/08326117B
Patent No. 5693491
GENERAL INFORMATION:
APPLICANT: BULLA, LEE A.
APPLICANT: JI, TAE
TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
TITLE OF INVENTION: TOXIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,117B
FILING DATE: 19-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 7112-0037.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-326-117B-14

Query Match 62.5%; Score 5; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8

DB 105 DTEVL 109

RESULT 6
US-08-982-129-14
Sequence 14, Application US/08982129
Patent No. 6007981
GENERAL INFORMATION:
APPLICANT: BULLA, LEE A.
APPLICANT: JI, TAE
TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
TITLE OF INVENTION: TOXIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,129
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,117
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 7112-0037.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-982-129-14

Query Match 62.5%; Score 5; DB 3; Length 122;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
DB 105 DTEVL 109

RESULT 7
US-08-928-443-1
Sequence 1, Application US/08928443
Patent No. 5785724
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN N-ACETYL TRANSFERASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,443
FILING DATE: HERWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0361 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT02
CLONE: 761783
US-08-928-443-1

Query Match 62.5%; Score 5; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SRDTE 6
11111
DB 157 SRDTE 161

RESULT 8
US-09-129-055-1
Sequence 1, Application US/09129055
Patent No. 6017744
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN N-ACETYL TRANSFERASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/129,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/928,443
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0361 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT02
CLONE: 761783
US-09-129-055-1

Query Match 62.5%; Score 5; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SRDTE 6
11111
DB 157 SRDTE 161

RESULT 9
US-08-318-837-7
Sequence 7, Application US/08318837
Patent No. 5981277
GENERAL INFORMATION:
APPLICANT: PRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE, VAN HEUVERSMYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,401,231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-837-7

Query Match 62.5%; Score 5; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
|||||
DB 193 DTEVL 197

RESULT 10
US-08-318-837-9
Sequence 9, Application US/08318837
Patent No. 5981277

GENERAL INFORMATION:
APPLICANT: FRANGEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY C
TITLE OF INVENTION: IMMUNOLOGY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSELLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318, 837
FILING DATE: 13-OCT-1994
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,401,231.3
FILING DATE: 30-APR-1992

ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSELLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-837-9

Query Match 62.5%; Score 5; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
|||||
DB 193 DTEVL 197

RESULT 11

US-08-078-683A-4
Sequence 4, Application US/08078683A
Patent No. 5486599

GENERAL INFORMATION:
APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton
APPLICANT: Kato, Masato
TITLE OF INVENTION: Construction and use of Synthetic
TITLE OF INVENTION: Constructs Encoding Syndecan
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078, 683A
FILING DATE: 17-JUN-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CME-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-078-683A-4

Query Match 62.5%; Score 5; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SRDTE 6
|||||
DB 82 SRDTE 86

RESULT 12
US-08-356-405-2
Sequence 2, Application US/08356405
Patent No. 5807691

GENERAL INFORMATION:
APPLICANT: Amlakky, No. 5807691irdine
APPLICANT: Boschert, Ursula
APPLICANT: Hen, Rene
APPLICANT: Plassat, Jean-Luc
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for These
TITLE OF INVENTION: Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/356,405
APPLICATION NUMBER: US/08/356,405
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: EX92004-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-405-2

Query Match 62.5%; Score 5; DB 1; Length 357;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DFEVL 8
DB 25 DFEVL 29

RESULT 13
US-08-806-263-2
Sequence 2, Application US/08806263
Patent No. 6221627
GENERAL INFORMATION:
APPLICANT: Sathe, Ganesh
APPLICANT: Van Horn, Stephanie
TITLE OF INVENTION: CDNA Clone HDPB130 That Encodes
TITLE OF INVENTION: A No. 6221627el Human 7-Transmembrane Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,263
FILING DATE: 24-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50003
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-806-263-2

Query Match 62.5%; Score 5; DB 4; Length 371;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRDTE 6
DB 332 SRDTE 336

RESULT 14
US-08-969-815-4
Sequence 4, Application US/08969815
Patent No. 6207412
GENERAL INFORMATION:
APPLICANT: Witte, Owen N.
APPLICANT: Meng, Zhigang
TITLE OF INVENTION: IDENTIFICATION OF A G PROTEIN-COUPLED
TITLE OF INVENTION: RECEPTOR TRANSCRIPTIONALLY REGULATED BY PROTEIN
TITLE OF INVENTION: TYROSINE KINASE SIGNALING IN HEMATOPOIETIC CELLS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,815
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: UCLAO15.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-969-815-4

Query Match 62.5%; Score 5; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 67;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRDTE 6
|||||
Db 341 SRDTE 345

RESULT 15
US-09-120-025-4
; Sequence 4, Application US/09120025
; Patent No. 6214562
; GENERAL INFORMATION:
; APPLICANT: Weng, Zhigang.
; APPLICANT: Wille, Owen N.
; TITLE OF INVENTION: TRANSCRIPTIONALLY REGULATED G PROTEIN-COUPLED
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,025
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/969,815
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartfeld, Neil S
; REGISTRATION NUMBER: 39,901
; REFERENCE/DOCKET NUMBER: UCLA015.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-120-025-4

Query Match 62.5%; Score 5; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRDTE 6
|||||
Db 341 SRDTE 345

Search completed: August 31, 2002, 12:20:20
Job time: 135 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 31, 2002, 12:20:25 ; Search time 10.33 Seconds

(without alignments)
29,966 Million cell updates/sec

Title: US-09-516-728-1

Perfect score: 8

Sequence: 1 QSRDEVL 8

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	8	100.0	1337 1 PRPJ_HUMAN	Q12913 homo sapien
2	6	75.0	499 1 CPDF_CANFA	Q29473 canis fami
3	6	75.0	500 1 CPDG_CAVPO	Q64403 cavia porce
4	5	62.5	68 1 P518_HUMAN	Q91156 homo sapien
5	5	62.5	88 1 E1B9_ADE07	P04490 human adeno
6	5	62.5	129 1 VH07_VACCV	P08586 vaccinia vi
7	5	62.5	146 1 VH07_VACCC	P20539 vaccinia vi
8	5	62.5	158 1 GLBD_CAUAR	P80017 caudina are
9	5	62.5	194 1 PUR1_LACCA	P35853 lactobacilli
10	5	62.5	217 1 VNS3_AHSV4	O64404 african hor
11	5	62.5	219 1 TSPD_CHLTR	O84468 chlamydia t
12	5	62.5	226 1 PYRE_KLUIA	O13474 kluyveromyc
13	5	62.5	235 1 TWFC_BACSU	P35639 bacillus su
14	5	62.5	238 1 DHSB_ECOLI	P07014 escherichia
15	5	62.5	271 1 RL5_DUNSA	O22608 dunaliella
16	5	62.5	286 1 CHER_ECOLI	P07364 escherichia
17	5	62.5	288 1 CHER_SALTY	P07801 salmone
18	5	62.5	298 1 HEMK_PASMD	O95n82 pasteurilla
19	5	62.5	309 1 SDC1_CRIGR	P47951 cricetulus
20	5	62.5	313 1 SDC1_RAT	P26260 rattus norv
21	5	62.5	325 1 FBP2_STRPU	P15216 strongyloce
22	5	62.5	334 1 Y456_MYCGE	P45666 mycoplasma
23	5	62.5	336 1 GUNA_MUMFL	P16169 rumiococcu
24	5	62.5	338 1 BZTA_RHOCA	O52663 rhodobacter
25	5	62.5	339 1 HRDC_STROCO	P18184 streptomyce
26	5	62.5	349 1 SCA3_MOUSE	O33609 mus musculu
27	5	62.5	357 1 SH5A_MOUSE	P30966 mus musculu
28	5	62.5	357 1 MORG_LACIA	Q9c192 lactococcus
29	5	62.5	381 1 HUPN_BRAJA	Q45247 bradyrhizob
30	5	62.5	419 1 IRK5_HUMAN	P48544 h g protein
31	5	62.5	419 1 IRK5_MOUSE	P48545 m g protein
32	5	62.5	419 1 IRK5_PIG	O02670 s g protein
33	5	62.5	419 1 IRK5_RAT	P48548 r g protein

34	5	62.5	430 1 AROA_MYCIE	Q9c13 mycobacteri
35	5	62.5	450 1 AROA_MYCRU	P22487 mycobacteri
36	5	62.5	476 1 PUR1_BACSU	P00497 bacillus su
37	5	62.5	477 1 P3_HUMAN	P09131 homo sapien
38	5	62.5	477 1 V12_PAPVE	P11327 european el
39	5	62.5	492 1 E1BL_ADE07	P03245 human adeno
40	5	62.5	493 1 AMYR_DROTE	O76260 drosophila
41	5	62.5	498 1 AMYR_AEGCO	O01396 aegilops co
42	5	62.5	498 1 ATPB_HORVU	P00828 hordeum vul
43	5	62.5	498 1 ATPB_WHEAT	P20858 triticum ae
44	5	62.5	518 1 HEMK_RICGR	Q9c13 rickettsia
45	5	62.5	519 1 PTA_HBLPU	Q92k04 helicobacte

ALIGNMENTS

RESULT	1	PRPJ_HUMAN	STANDARD:	PRT: 1337 AA.
ID	PRPJ_HUMAN	Q12913; 015255;		
AC	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)			
DE	(HPTP eta) (Density enhanced phosphatase-1) (DEP-1) (CD148 antigen).			
GN	PRPJ OR DEP1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95024024; PubMed=7937872;			
RA	Oestman A., Yang Q., Tomks N.K.;			
RT	"Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,			
RT	is enhanced with increasing cell density."			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95086212; PubMed=7994032;			
RA	Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;			
RT	"Molecular cloning, characterization, and chromosomal localization of			
RT	a novel protein-tyrosine phosphatase, HPTP eta."			
RL	Blood 84:4186-4194(1994).			
CC	-1- FUNCTION: MAY CONTRIBUTE TO THE MECHANISM OF CONTRACT INHIBITION OF			
CC	CELL GROWTH.			
CC	-1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- PTM: N- AND O-GLYCOSYLATED.			
CC	-1- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CD148 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib.ch).			
CC	-----			
CC	EMBL: U10886; AAB36687.1; -;			
CC	EMBL: D37781; BAA07035.1; -;			
CC	HSSP: P18052; 1YFO.			
CC	MIM: 600925; -;			
CC	InterPro: IPR003961; FN.III.			
CC	InterPro: IPR000387; TYR_phosphatase.			
CC	InterPro: IPR000242; TYR_prot_phphatase.			
CC	Pfam: PF00041; fn3; 5.			
CC	Pfam: PF00102; Y_phosphatase; 1.			

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DR PRINTS; PRO0700; PRTYPHPHTASE.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Signal; Glycoprotein; Transmembrane; Repeat; Hydrolase.
FT SIGNAL 1 35
FT CHAIN 36 1337
FT DOMAIN 36 975
FT TRASMEM 976 996
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT FIBRONECTIN TYPE-III 1.
FT FIBRONECTIN TYPE-III 2.
FT FIBRONECTIN TYPE-III 3.
FT FIBRONECTIN TYPE-III 4.
FT FIBRONECTIN TYPE-III 5.
FT DOMAIN 626 710
FT DOMAIN 1065 1337
FT ACT_SITE 1239 1239
FT CARBOHYD 72 72
FT CARBOHYD 82 82
FT CARBOHYD 93 93
FT CARBOHYD 104 104
FT CARBOHYD 142 142
FT CARBOHYD 172 172
FT CARBOHYD 192 192
FT CARBOHYD 231 231
FT CARBOHYD 258 258
FT CARBOHYD 278 278
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FT CARBOHYD 351 351
FT CARBOHYD 376 376
FT CARBOHYD 391 391
FT CARBOHYD 396 396
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FT CARBOHYD 536 536
FT CARBOHYD 582 582
FT CARBOHYD 603 603
FT CARBOHYD 618 618
FT CARBOHYD 628 628
FT CARBOHYD 637 637
FT CARBOHYD 666 666
FT CARBOHYD 669 669
FT CARBOHYD 751 751
FT CARBOHYD 772 772
FT CARBOHYD 784 784
FT CARBOHYD 790 790
FT CARBOHYD 824 824
FT CARBOHYD 910 910
FT CARBOHYD 937 937
FT CONFLICT 261 261
FT CONFLICT 918 929
SQ SEQUENCE 1337 AA; 145985 MW; E686DE6D1F64236E CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 1; Length 1337;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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DT 15-DEC-1998 (rel. 37, Last annotation update)
DE Cytochrome P450 2D15 (EC 1.14.14.1) (CYP2D15) (P450 DUT2).
GN CYP2D15.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver.
RX MEDLINE=95305574; PubMed=7786018;
RA Sakamoto K., Kirita S., Baba T., Nakamura Y., Yamazoe Y., Kato R.,
RA Takahana A., Matsubara T.;
RT "A new cytochrome P450 form belonging to the CYP2D in dog liver
RT microsomes: purification, cDNA cloning, and enzyme
RT characterization."
RL Arch. Biochem. Biophys. 319:372-382(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BEAGLE;
RX MEDLINE=98162950; PubMed=9504424;
RA Tasaki T., Nakamura A., Itoh S., Ohashi K., Yamamoto Y., Masuda M.,
RA Iwata H., Kazusaka A., Kametaki T., Fujita S.;
RT "Expression and characterization of dog CYP2D15 using baculovirus
RT expression system."
RL J. Biochem. 123:162-168(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98389575; PubMed=9721180;
RA Rousset F., Daignan D.B., Lawton M.P., Obach R.S., Strick C.A.,
RA Tweedie D.J.;
RT "Expression and characterization of canine cytochrome P450 2D15."
RL Arch. Biochem. Biophys. 357:27-36(1998).
CC -1- FUNCTION: HIGH ACTIVITY FOR THE HYDROXYLATION OF BUNITROL AND
CC IMPRAMINE: LOW ACTIVITY ON DEBRISOQUINE.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) -> ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: LIVER. ALSO DETECTED IN SEVERAL OTHER TISSUES.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC
CC EMBL; D17397; BAA04220.1; -.
CC EMBL; AB004268; BAA20357.1; -.
CC HSSP; F00179; 1D76.
CC InterPro: IPR001128; CYP_P450.
CC Pfam; PF00067; P450; 1.
DR PRINTS; PRO0385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT INIT MET 0 0
FT BINDING 445 445 HEME (BY SIMILARITY).
FT SEQUENCE 499 AA; 56301 MW; 27E352B5B309E7F1 CRC64;

Query Match
Best Local Similarity 75.0%; Score 6; DB 1; Length 499;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CPDG_CAVPO STANDARD: PRT: 500 AA.
 ID CPGD_CAVPO 064403; 054866;
 AC 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cytochrome P450 2D16 (EC 1.14.14.1) (CYP1D16).
 GN CYP2D16.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriicongnath; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-38.
 RC STRAIN=13; TISSUE=Adrenal cortex;
 RX MEDLINE=95251703; PubMed=7733969;
 RA Jiang Q., Voigt J.M., Colby H.D.;
 RT "Molecular cloning and sequencing of a guinea pig cytochrome P4502D
 RT (CYP2D16): high level expression in adrenal microsomes."
 RL Biochem. Biophys. Res. Commun. 209:1149-1156(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HARTLEY WHITE; TISSUE=Adrenal gland;
 RA Sun Y., Voigt J.M., Pierce J.C., Colby H.D.;
 RT "The gene sequence of a xenobiotic metabolism-related cytochrome P450
 RT isozyme (CYP2D16) in guinea pig adrenal gland."
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
 CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
 CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
 CC ACIDS, AND XENOBIOTICS.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) -> ROH +
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE INNER ZONE OF
 CC THE ADRENAL CORTEX.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; U21486; AAA68479.1; -;
 CC DR EMBL; AF020345; AAB94568.1; -;
 CC DR InterPro: IPR001128; Cyt_P450.
 CC DR Pfam: PF00067; P450; 1.
 CC DR PRINTS: PR00385; P450.
 CC DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 CC KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 CC KW Microsome; Endoplasmic reticulum.
 CC FT DOMAIN 81 84 POLY-VAL.
 CC FT BINDING 446 446 HEME (BY SIMILARITY).
 CC FT CONFLICT 123 123 I -> V (IN REF. 2).
 CC FT CONFLICT 127 127 Y -> N (IN REF. 2).
 CC FT CONFLICT 148 148 G -> R (IN REF. 2).
 CC SO SEQUENCE 500 AA; 55800 MW; 2429247E49BF6B24 CRC64;

Query Match 75.0%; Score 6; DB 1; Length 500;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SDRTEV 7
 Db 382 SDRTEV 387

RESULT 4

P518_HUMAN STANDARD: PRT: 68 AA.
 ID P518_HUMAN 090156;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein P000518.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RA Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,
 RA Liu M., He F.;
 RT "Functional prediction of the coding sequences of 50 new genes deduced
 RT by analysis of cDNA clones from human fetal liver."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; AF090934; AAF24048.1; -;
 CC SO SEQUENCE 68 AA; 7791 MW; DDC6B78EC2981B99 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 68;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QSRDT 5
 Db 2 QSRDT 6

RESULT 5
 EIB9_ADE07 STANDARD: PRT: 88 AA.
 ID EIB9_ADE07
 AC P04490;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE Early E1B 9 kDa protein.
 OS Human adenovirus type 7.
 CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 CC OX NCBI_TaxID=10519;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=GOMEN;
 CC RX MEDLINE=83028529; PubMed=6290319;
 CC RA Dijkema R., Dekker B.M.M., van Ormondt H.;
 CC RT "Gene organization of the transforming region of adenovirus type 7
 CC RT DNA."
 CC RL Gene 18:143-156(1982).
 CC -1- MISCELLANEOUS: RESIDUES 1-86 ARE IDENTICAL WITH RESIDUES 1-86 OF
 CC THE E1B 55K PROTEIN.
 CC -----

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DR EMBL; X03000; CAA26761.1; -;
 PIR; A03811; WMAD9.

KW Early protein.
SQ SEQUENCE 88 AA; 9017 MW; 6E5CDC749DB8EFP8 CRC64;
Query Match
Best Local Similarity 62.5%; Score 5; DB 1; Length 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRDTE 6
DB 44 SRDTE 48
RESULT 6
VH07_VACCV STANDARD; PRT; 129 AA.
ID P08586;
AC 01-AUG-1988 (Rel. 08; Created)
DT 01-AUG-1988 (Rel. 08; Last sequence update)
DE Late protein H7 (Protein H8) (Fragment).
GN H7R.
OS Vaccinia virus (strain WR).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87036903; PubMed=3021979;
RA Rosel J.L., Earl P.L., Weir J.P., Moss B.;
RT "Conserved TAAATG sequence at the transcriptional and translational
initiation sites of vaccinia virus late genes deduced by structural
and functional analysis of the HindIII H genome fragment.";
RL J. Virol. 60:436-449(1986).
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES H7 FAMILY.

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CC
DR EMBL; M13209; AAB59843.1; -.
DR PIR; H24481; QOVZ88.
KW Late protein.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 15003 MW; F280258FCD885121 CRC64;
Query Match
Best Local Similarity 62.5%; Score 5; DB 1; Length 129;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRDTE 6
DB 123 SRDTE 127
RESULT 7
VH07_VACCV STANDARD; PRT; 146 AA.
ID P20539;
AC 01-FEB-1991 (Rel. 17; Created)
DT 01-FEB-1991 (Rel. 17; Last sequence update)
DE 16-OCT-2001 (Rel. 40; Last annotation update)
GN Late protein H7.
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10249;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266(1990).
RN [2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RL Virology 179:517-563(1990).
CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES H7 FAMILY.

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CC
DR EMBL; M35027; AAA48094.1; -.
DR PIR; G42514; QOVZ28.
KW Late protein.
SQ SEQUENCE 146 AA; 16912 MW; 1DC1B502E7A07E58 CRC64;
Query Match
Best Local Similarity 62.5%; Score 5; DB 1; Length 146;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRDTE 6
DB 123 SRDTE 127
RESULT 8
GLBD_CAVAR STANDARD; PRT; 158 AA.
ID P80017;
AC 01-MAY-1991 (Rel. 18; Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DE 15-JUL-1998 (Rel. 36; Last annotation update)
GN Globin D, coelomic.
OS Caudina arenicola (sea cucumber) (Molipadia arenicola).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Holothuroidea; Apodacea; Molipadiida; Caudinidae; Caudina.
OX NCBI_TaxID=7698;
RN [1]
RP SEQUENCE.
RX TISSUE=Coelomic fluid;
MEDLINE=91265540; PubMed=2049384;
MAURI F., OMAAS J., DAVIDSON L., WHITFIELD C., KITTO G.B.;
RT "Amino acid sequence of a globin from the sea cucumber Caudina
(Molipadia) arenicola.";
RL Biochim. Biophys. Acta 1078:63-67(1991).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS), AND REVISIONS.
RA MITCHELL D.T., ERNST S.R., HACKERT M.L.;
RT "X-ray structure determination of a dimeric hemoglobin from Caudina
arenicola.";
RL Acta Crystallogr. D 51:760-766(1995).
CC -1- SUBUNIT: HOMODIMER.
CC -1- MISCELLANEOUS: CAUDINA ARENICOLA COELOMOCYTES CONTAIN FOUR
HEMOGLOBIN CHAINS LABELED A, B, C, D.
CC -1- SIMILARITY: STRONG, TO C.ARENICOLA GLOBIN C AND P.CHILENSIS GLOBIN
I.
DR PIR; S15979; S15979.
DR PDB; 1HLM; 07-FEB-95.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.

DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Acetylation;
3D-structure.
FT MOD_RES 1 1 ACETYLATION.
FT METAL 73 73 IRON (HEME DISTAL LIGAND).
FT METAL 104 104 IRON (HEME PROXIMAL LIGAND).
FT CONFLICT 2 4 ATQ -> QAT (IN REF. 1).
FT CONFLICT 48 48 T -> W (IN REF. 1).
SQ SEQUENCE 158 AA; 17675 MW; 363BC16BD9661352 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
Db 89 DTEVL 93

RESULT 9
PURL_IACCA STANDARD; PRT; 194 AA.
AC P35853;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Adiphosphoribosyltransferase precursor (EC 2.4.2.14) (Glutamine
phosphoribosylpyrophosphate amidotransferase) (ATPase) (GPATase)
DE (fragment).
GN PURF.
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
CC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93012962; PubMed=1398079;
RX Gu Z.-M., Martindale D.W., Lee B.H.;
RT "Isolation and complete sequence of the purl gene encoding FGAM
synthase II in Lactobacillus casei.";
RL Gene 119:123-126(1992).
RN [2]
RP ERRATUM.
RX MEDLINE=94040790; PubMed=8224889;
RA Gu Z.-M., Martindale D.W., Lee B.H.;
RL Gene 133:147-147(1993).
CC -1- CATALYTIC ACTIVITY: 5-phospho-beta-D-riboylamine + diphosphate +
L-glutamate = L-glutamine + 5-phospho-alpha-D-ribose 1-diphosphate +
H(2)O.
CC -1- PATHWAY: FIRST STEP IN DE NOVO PURINE BIOSYNTHESIS.
CC -1- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
AMIDOTRANSFERASES.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO THE
PRIME/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL; M85265; AAC36948.1; -.
DR PIR; PC1136; PC1136.
DR HSSP; P00497; 1A00.
DR MEROPS; C44.001; -.
DR InterPro: IPR000583; GATase_2.
DR InterPro: IPR002375; Pur_Pyl_Pr_Transf.
DR Pfam; PF00310; GATase_2; 1.
DR PROSITE; PS00103; Pur_Pyl_Pr_Transfer; PARTIAL.
DR PROSITE; PS00443; GATase_Type_1; 1.

KW Purine biosynthesis; Transferase; Glycosyltransferase.
FT PROPEP 1 11 BY SIMILARITY.
FT CHAIN 12 >194 AMIDOPHOSPHORIBOSYLTRANSFERASE.
FT ACT_SITE 12 12 GATASE (INVOLVED IN SUBSTRATE BINDING AND
CATALYSIS) (BY SIMILARITY).
FT NON_TER 194 194
SQ SEQUENCE 194 AA; 21144 MW; 4A788CB5365D5BC CRC64;

Query Match 62.5%; Score 5; DB 1; Length 194;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
Db 138 DTEVL 142

RESULT 10
VNS3_AHSV4 STANDARD; PRT; 217 AA.
AC Q64904;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nonstructural protein NS3 [Contains: Nonstructural protein NS3A].
GN S10.
OS African horse sickness virus 4 (AHSV-4) (African horse sickness virus
(serotype 4)).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=36421;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95066364; PubMed=7975880;
RA de Sa R., Zellner M., Grudman M.J.;
RT "Phylogenetic analysis of segment 10 from African horsesickness virus
and cognate genes from other orbiviruses.";
RL Virus Res. 33:157-165(1994).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE RELEASE OF VIRIONS FROM INFECTED
CELLS.
CC -----
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES NS3 FAMILY.
CC -----
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CC -----
DR EMBL; U02712; AAA21527.1; -.
DR InterPro: IPR002565; Orbl_NS3.
DR Pfam; PF01616; Orbl_NS3; 1.
DR ProDom: PD003183; Orbl_NS3; 1.
KW Nonstructural protein.
FT CHAIN 1 217 NONSTRUCTURAL PROTEIN NS3.
FT CHAIN 12 217 NONSTRUCTURAL PROTEIN NS3A.
SQ SEQUENCE 217 AA; 23663 MW; 4CFD0C4E0B9612P4 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
Db 204 DTEVL 208

RESULT 11
ISPDC_HLHTR STANDARD; PRT; 219 AA.
AC O84468;

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DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 2-C-methyl-D-erythritol 4-phosphoryltransferase (EC 2.7.7.60)
DE (4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
DE cytidyllyltransferase) (MCT).
GN ISPD OR C7462.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/W-3/CX;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RT Science 282:754-759(1998).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-
CC D-ERYTHRITOL FROM CDP AND 2C-METHYL-D-ERYTHRITOL 4-PHOSPHATE (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: CDP + 2-C-methyl-D-erythritol 4-phosphate =
CC diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third
CC step.
CC -1- SIMILARITY: BELONGS TO THE ISPD FAMILY.
CC -----
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CC -----
CC
CC EMBL; AE001320; AAC68062.1; -.
CC InterPro: IPR001228; ISPD.
CC Pfam; PF01128; UPF0007; 1.
CC PROSITE; PS01295; ISPD; 1.
CC Transferrase; Nucleotidyltransferase; Isoprene biosynthesis;
CC Complete proteome.
CC KW SEQUENCE 219 AA; 24168 MW; 45C69BF8250364D CRC64;
CC
CC
CC Query Match 62.5%; Score 5; DB 1; Length 219;
CC Best Local Similarity 100.0%; Pred. No. 36;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC
CC QY 4 DREVL 8
CC [1111]
CC DB 155 DREVL 159
CC
CC
CC RESULT 12
CC PYRE_KLUOA STANDARD; PRT; 226 AA.
CC ID 013474;
CC AC 013474;
CC DT 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE Orotate phosphoribosyltransferase (EC 2.4.2.10) (OMPPASE) (OPRT).
CC GN URA5.
CC OS Kluyveromyces fragilis (Yeast).
CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
CC OX NCBI_TaxID=28985;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=CBS 683;
CC RA Bal X., Larsen M., Meinhardt F.;
CC Submitted (SEP-1997) to the EMBL/GenBank/DDA databases.

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CC -1- CATALYTIC ACTIVITY: Orotidine 5'-phosphate + diphosphate -> orotate
CC + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: FIFTH STEP IN PYRIMIDINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
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CC -----
CC
CC EMBL; AJ001358; CAA04694.1; -.
CC HSSP; P08870; ISTO.
CC InterPro: IPR000836; Pribosyltran.
CC DR InterPro; IPR002375; pur_pyr_pr_transf.
CC DR Pfam; PF00156; Pribosyltran; 1.
CC DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
CC KW Pyrimidine biosynthesis; Transferase; Glycosyltransferase.
CC ACT SITE 110 110 BY SIMILARITY.
CC FT SEQUENCE 226 AA; 24815 MW; E69FE06DDBC65B0 CRC64;
CC
CC
CC Query Match 62.5%; Score 5; DB 1; Length 226;
CC Best Local Similarity 100.0%; Pred. No. 37;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC
CC QY 4 DREVL 8
CC [1111]
CC DB 172 DREVL 176
CC
CC
CC RESULT 13
CC YWFC_BACSU STANDARD; PRT; 235 AA.
CC ID 039639;
CC AC 01-FEB-1995 (Rel. 31, Created)
CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Hypothetical 26.8 kDa protein in ROCC-PTA intergenic region.
CC GN YWFC OR IRA-81D.
CC OS Bacillus subtilis.
CC OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus.
CC OX NCBI_TaxID=1423;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=168;
CC RX MEDLINE=95020537; PubMed=7934828;
CC RA Glaser P., Kunst F., Arnold M., Coudart M.P., Gonzales M.,
CC Hullo M.F., Ionescu M., Imbichinsky B., Marcelino L., Moszer I.,
CC Prescan E., Santana M., Schneider E., Schweizer J., Vertes A.,
CC Rapoport G., Danchin A.;
CC RA "Bacillus subtilis genome project: cloning and sequencing of the 97
CC kb region from 325 degrees to 333 degrees."
CC Mol. Microbiol. 10:371-384(1993).
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CC -----
CC
CC EMBL; X73124; CAA51637.1; -.
CC DR EMBL; Z99123; CAB15800.1; -.
CC DR PIR; S39736; S39736.
CC DR Subtilist; BG10627; YWFC.
CC KW Hypothetical protein; Complete proteome.
CC SEQUENCE 235 AA; 26839 MW; 9A9A1608148D0FA6 CRC64;

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Query Match 62.5%; Score 5; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
 11111
 DB 33 DTEVL 37

RESULT 14
 DMSB_ECOLI STANDARD; PRT; 238 AA.
 ID DMSB_ECOLI
 AC P07014;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Succinate dehydrogenase iron-sulfur protein (Ec 1.3.99.1).
 GN SDHB OR B0724.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 OX [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=85046453; PubMed=6388571;
 RA Darlison M.G., Guest J.R.;
 RT "Nucleotide sequence encoding the iron-sulphur protein subunit of the
 RL succinate dehydrogenase of Escherichia coli.";
 RL Biochem. J. 223:507-517(1984).
 [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blather F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 [3]
 RC SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sanpei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horinouchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 [4]
 RC SEQUENCE OF 231-238 FROM N.A.
 RX MEDLINE=84236168; PubMed=6376123;
 RA Darlison M.G., Spencer M.E., Guest J.R.;
 RT "Nucleotide sequence of the suca gene encoding the 2-oxoglutarate
 RT dehydrogenase of Escherichia coli K12.";
 RL Eur. J. Biochem. 141:351-359(1984).
 [5]
 RP SEQUENCE OF 1-11.
 RP STRAIN=K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 CC -
 CC FUNCTION: TWO DISTINCT, MEMBRANE-BOUND, FAD-CONTAINING ENZYMES ARE
 CC RESPONSIBLE FOR THE CATALYSIS OF FUMARATE AND SUCCINATE
 CC INTERCONVERSION; THE FUMARATE REDUCTASE IS USED IN ANAEROBIC

CC GROWTH, AND THE SUCCINATE DEHYDROGENASE IS USED IN AEROBIC GROWTH.
 CC -1 CATALYTIC ACTIVITY: Succinate + acceptor = fumarate + reduced
 CC acceptor.
 CC -1 COFACTOR: BINDS THREE DIFFERENT IRON-SULFUR CLUSTERS: A 2FE-2S,
 CC A 3FE-4S AND A 4FE-4S.
 CC -1 PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1 SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING FOUR SUBUNITS: A
 CC FLAVOPROTEIN, AN IRON-SULFUR, CYTOCHROME B-556, AND AN HYDROPHOBIC
 CC ANCHOR PROTEIN.
 CC -1 SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
 CC 'PLANT-TYPE' 2FE-2S AND 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
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 CC -----

DR EMBL; J01619; AAA23896.1; -;
 DR EMBL; X01070; CAA25534.1; -;
 DR EMBL; AE000175; AAC73818.1; -;
 DR EMBL; D90711; BAA35391.1; -;
 DR EMBL; X00661; CAA25279.1; -;
 DR PIR; A28837; DEECST.
 DR HSSP; P00364; IFUM.
 DR Ecogene; EG10932; sdhB.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR001041; Ferredoxin.
 DR Pfam; PF00111; fer2; 1.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
 KW Tricarboxylic acid cycle; Iron-sulfur; Oxidoreductase;
 KW Electron transport; 3Fe-4S; 4Fe-4S; Complete proteome;
 FT METAL 55
 FT METAL 55
 FT METAL 60
 FT METAL 75
 FT METAL 149
 FT METAL 152
 FT METAL 155
 FT METAL 159
 FT METAL 206
 FT METAL 212
 FT METAL 216
 SQ SEQUENCE 238 AA; 26770 MW; 226F6C55F5AC35A CMC64;

Query Match 62.5%; Score 5; DB 1; Length 238;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SRDTE 6
 11111
 DB 185 SRDTE 189

RESULT 15
 RL5_DUNSA STANDARD; PRT; 271 AA.
 ID RL5_DUNSA
 AC O22608;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 60S ribosomal protein L5.
 GN RPL5 OR DSRP1.
 OS Dunaliella salina.
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 CC Dunalaliaceae; Dunalialla.
 OX NCBI_TaxID=3046;
 OX [1]
 RP SEQUENCE FROM N.A.
 RP KO J.H.; Lee S.H.;
 RA "A cDNA encodes a protein sequence homologous to the eukaryotic

RT ribosomal 5S RNA-binding protein from Dunaliella salina.;
Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF028833; AAB84056.1; -;
DR InterPro; IPR001149; Ribosomal_L18p.
DR Pfam; PF00861; Ribosomal_L18p; 1.
DR PRINTS; PR00058; RIBOSOMAL15.
DR ProDom; PD001394; Ribosomal_L18p; 1.
KW Ribosomal protein; rRNA-binding.
SQ SEQUENCE 271 AA; 31218 MW; 482F53833D33B57E CRC64;

Query Match 62.5%; Score 5; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 DREVL 8
|||||
Db 189 DREVL 193

Search completed: August 31, 2002, 12:23:58
Job time: 213 sec

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 OSRDTEVL 8
|||||

DB 324 OSRDTEVL 331

RESULT 2

JC4157

Cytochrome P450 2D, endoplasmic reticulum - dog
N:Alternate names: cytochrome P450 2D, microsomal

C:Species: Canis lupus familiaris (dog)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C:Accession: JC4157; S65962; S65898

R:Jiang, Q.; Voigt, J.M.; Colby, H.D.

Biochem. Biophys. Res. Commun. 209, 1149-1156, 1995

A:Title: Molecular cloning and sequencing of a guinea pig cytochrome P4502D (CYP2D16): h

A:Reference number: JC4153; MUID:95251703

A:Accession: JC4157

A:Cross-references: GB:U21486; NID:9862481

A:Residues: 1-500 <JIA>

A:Status: preliminary

A:Residues: 1-500 <SAK>

A:Cross-references: EMBL:DJ7397; NID:9397824; PIDN:BA04220.1; PID:9397825

A:Accession: S65898

A:Molecule type: protein

A:Residues: 2-37, 'X', 39 <SAW>

A:Comment: This protein is a member of the CYP2D subfamily, it represents the isozyme as

C:Genetics:

A:Gene: CYP2D15

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: adrenal gland; chromoprotein; endoplasmic reticulum; heme; iron; metalloprot

F:305-468/Domain: cytochrome P450 homology <P45>

F:446/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

Best Local Similarity 75.0%; Score 6; DB 1; Length 500;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SRDTEV 7
|||||

DB 382 SRDTEV 387

RESULT 3

JC4153

Cytochrome P450 2D16, CYP2D16 - guinea pig

N:Contains: oxidoreductase (EC 1.-.-.-)

C:Species: Cavia porcellus (guinea pig)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000

C:Accession: JC4153; PC4052

R:Jiang, Q.; Voigt, J.M.; Colby, H.D.

Biochem. Biophys. Res. Commun. 209, 1149-1156, 1995

A:Title: Molecular cloning and sequencing of a guinea pig cytochrome P4502D (CYP2D16): h

A:Reference number: JC4153; MUID:95251703

A:Accession: JC4153

A:Molecule type: mRNA

A:Residues: 1-500 <JIA>

A:Cross-references: GB:U21486; NID:9862481; PIDN:AAA68479.1; PID:9862482

A:Accession: PC4052

A:Molecule type: protein

A:Residues: 1-37 <JIA>

C:Comment: This protein is a member of the CYP2D subfamily, it represents the isozyme as

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

Query Match

Best Local Similarity 62.5%; Score 5; DB 2; Length 93;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 OSRDTEV 5
|||||

DB 71 OSRDTEV 75

RESULT 6

C:Keywords: adrenal gland; chromoprotein; heme; iron; metalloprotein; microsome; oxid
F:305-468/Domain: cytochrome P450 homology <P45>
F:496/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

Best Local Similarity 75.0%; Score 6; DB 1; Length 500;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SRDTEV 7
|||||

DB 382 SRDTEV 387

RESULT 4

MMAD9

early E1B 9K protein I - human adenovirus 7

C:Species: Mastadenovirus h7 (human adenovirus 7)

A:Note: host Homo sapiens (man)

C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999

C:Accession: A03811

R:DiJkema, R.; Dekker, B.M.M.; van Ormondt, H.

Gene 18, 143-156, 1982

A:Title: Gene organization of the transforming region of adenovirus type 7 DNA.

A:Reference number: A91494; MUID:83028529

A:Accession: A03811

A:Molecule type: DNA

A:Residues: 1-88 <DIJ>

A:Cross-references: GB:X03000; GB:J01981; GB:J01982; GB:J01983; GB:J01984; GB:J01985;

520

C:Comment: Residues 1-86 are identical with residues 1-86 of the E1B 53K protein I.

C:Superfamily: adenovirus early E1B protein I

C:Keywords: early protein

Query Match

Best Local Similarity 62.5%; Score 5; DB 1; Length 88;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SRDTE 6
|||||

DB 44 SRDTE 48

RESULT 5

A41975

major histocompatibility complex class I alpha 3 domain homolog - shark (Triakis scyll

C:Species: Triakis scyllium

C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 26-Aug-1999

C:Accession: A41975

R:Hashimoto, K.; Kurosawa, Y.

Proc. Natl. Acad. Sci. U.S.A. 89, 2209-2212, 1992

A:Title: Identification of a shark sequence resembling the major histocompatibility c

A:Reference number: A41975; MUID:92196087

A:Accession: A41975

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-93 <HSA>

A:Cross-references: GB:M85291; NID:9213922

A:Note: sequence extracted from NCBI backbone (NCBIN:88077, NCBIR:88079); this ORF is

A:Note: the source is designated as Triakis scyllia

Query Match

Best Local Similarity 62.5%; Score 5; DB 2; Length 93;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 OSRDTEV 5
|||||

DB 71 OSRDTEV 75

RESULT 6

S55691
keratin type I (clone Jn7-4) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Oct-1995 #sequence_revision 07-Feb-1997 #text_change 10-Dec-1999
C:Accession: S55691
R:Adact, N.; Ito, T.; Koga, C.; Kito, K.; Sakaki, Y.; Shikawa, K.
Biochim. Biophys. Acta 1262, 43-51, 1995
A:Title: Differential display analysis of gene expression in developing embryos of Xenopus
A:Reference number: S55691; MUID:95290493
A:Accession: S55691
A:Molecule type: mRNA
A:Residues: 1-105 <ADA>
A:Cross-references: EMBL:S76089, NID:g999222; PIDD:AA834522.1; PID:g999223
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament

Query Match 62.5%; Score 5; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DTEVL 8
DB 99 DTEVL 103

RESULT 7
S07258
helix-destabilizing protein - plasmid RK2
N:Alternate names: san protein; single-stranded DNA-binding protein ssb
C:Species: plasmid RK2
C:Date: 18-Feb-1994 #sequence_revision 17-May-1996 #text_change 03-Dec-1999
C:Accession: S07258; A44020; S26289
R:Smith, C.A.; Thomas, C.M.
J. Mol. Biol. 175, 251-262, 1984
A:Title: Nucleotide sequence of the trfA gene of broad host-range plasmid RK2.
A:Reference number: S07258; MUID:84216332
A:Accession: S07258
A:Molecule type: DNA
A:Residues: 1-116 <SMT>
A:Cross-references: EMBL:X00713, NID:g45775; PIDD:CAA23305.1; PID:g45776
A:Note: the authors translated the codon CAC for residue 64 as Gln
R:Lessl, M.; Balzer, D.; Pansegrau, W.; Lanka, E.
J. Biol. Chem. 267, 20471-20480, 1992
A:Title: Sequence similarities between the Rpl Tra2 and the T1 VirB region strongly support
A:Reference number: A44020; MUID:92015931
A:Contents: incompatibility group P
A:Accession: A44020
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-37 <LES>
A:Note: sequence extracted from NCBI backbone (NCBI:P115752)
R:Jagura-Burdzy, G.; Khanim, F.; Smith, C.A.; Thomas, C.M.
Nucleic Acids Res. 20, 3939-3944, 1992
A:Title: Crossstalk between plasmid vegetative replication and conjugative transfer: repl
A:Reference number: S26289; MUID:92375675
A:Contents: annotation
C:Genetics:
A:Genome: plasmid RK2
C:Superfamily: single-stranded DNA-binding protein; single-stranded DNA-binding protein
C:Keywords: single-stranded DNA binding
F:19-95/Domain: single-stranded DNA-binding protein homology <SSD>

Query Match 62.5%; Score 5; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RDTFV 7
DB 14 RDTFV 18

RESULT 8
T17967
EBV1 protein homolog A465R - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17967
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: T17967
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-118 <GRA>
A:Cross-references: EMBL:U42580; NID:g4028896; PIDD:AA096832.1
A:Experimental source: specific host Chlorella strain NC64
C:Genetics:
A:Note: A465R

Query Match 62.5%; Score 5; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSRDT 5
DB 77 QSRDT 81

RESULT 9
Q0VZH8
H8 protein - vaccinia virus (strain WR) (fragment)
C:Species: vaccinia virus
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
C:Accession: H24481
R:Rosel, J.U.; Earl, P.L.; Weir, J.P.; Moss, B.
J. Virol. 60, 436-449, 1986
A:Title: Conserved TAAATG sequence at the transcriptional and translational initiation
A:Reference number: A93022; MUID:87036903
A:Accession: H24481
A:Molecule type: DNA
A:Residues: 1-129 <ROS>
A:Cross-references: GB:M13209; NID:g335739; PIDD:AA859843.1; PID:g335746
C:Superfamily: vaccinia virus H8 protein
C:Keywords: late protein

Query Match 62.5%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRDTE 6
DB 123 SRDTE 127

RESULT 10
Q0VZ28
H8 protein - vaccinia virus (strain Copenhagen)
N:Alternate names: H7R protein
C:Species: vaccinia virus
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
C:Accession: G42514
R:Johnson, G.P.
submitted to GenBank, June 1990
A:Reference number: A33172
A:Accession: G42514
A:Molecule type: DNA
A:Residues: 1-146 <JOH>
A:Cross-references: GB:M5027; NID:g335317; PIDD:AAA48094.1; PID:g335442.
C:Superfamily: vaccinia virus H8 protein
C:Keywords: late protein

Query Match 62.5%; Score 5; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SRPTE 6
|||||
DB 123 SRPTE 127

RESULT 11
T37373
probable 17K protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A:Virus: strain Ankara
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T37373
R:Antoine, G.; Schelfinger, F.; Falkner, F.G.; Dörner, F.
Submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
A:Reference number: 220877
A:Accession: T37373
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-146 <ANT>
A:Cross-references: EMBL:U94848; PIDN:AAB96510.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA097R
C:Superfamily: vaccinia virus H8 protein

Query Match 62.5%; Score 5; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SRPTE 6
|||||
DB 123 SRPTE 127

RESULT 12
S72241
dynein heavy chain 3 - Chlamydomonas reinhardtii (fragment)
C:Species: Chlamydomonas reinhardtii
C:Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000
C:Accession: S72241
R:Porter, M.E.; Knott, J.A.; Myster, S.H.; Farlow, S.J.
Genetics 144, 569-585, 1996
A:Title: The dynein gene family in Chlamydomonas reinhardtii.
A:Reference number: S72239; MUID:97044450
A:Accession: S72241
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-147 <POR>
A:Cross-references: EMBL:U61366; NID:g1663739; PIDN:AAC49516.1; PID:g1663740
C:Genetics:
A:Introns: 44/1; 109/3

Query Match 62.5%; Score 5; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DREVL 8
|||||
DB 99 DREVL 103

RESULT 13
A12245
hypothetical protein al13520 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.

A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: A12245
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: A12245
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-154 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA075219.1; PID:g17132653; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: al13520

Query Match 62.5%; Score 5; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSRDT 5
|||||
DB 134 OSRDT 138

RESULT 14
S15979
hemoglobin beta chain - sea cucumber (Caudina arenicola)
M:Alternate names: D globin
C:Species: Caudina arenicola
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 19-May-2000
C:Accession: S15979
R:Mauri, F.; Omasas, J.; Davidson, L.; Whittall, C.; Kitto, G.B.
Biochim. Biophys. Acta 1078, 63-67, 1991
A:Title: Amino acid sequence of a globin from the sea cucumber Caudina (Molpadia) are
A:Reference number: S15979; MUID:91265540
A:Accession: S15979
A:Molecule type: protein
A:Residues: 1-158 <BIO>
A:Superfamily: globin; globin homology
C:Keywords: blocked amino end; blood; chromoprotein; dimer; erythrocyte; heme; iron;
F:12-157/Domain: globin homology <GLB>
F:1/Modified site: blocked amino end (Gly) (probably acetylated) #status experimental
F:173/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:104/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DREVL 8
|||||
DB 89 DREVL 93

RESULT 15
B84098
acetyltransferase BH3586 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: B84098
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujl, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: B84098
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <STO>
A:Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA07305.1; GSPDB:G

A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3586

Query Match 62.5%; Score 5; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 2 SRDTE 6
|||||
Db 2 SRDTE 6

Search completed: August 31, 2002, 12:20:42
Job time: 122 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 31, 2002, 12:16:10 ; Search time 29.86 Seconds
(without alignments)
29.759 Million cell updates/sec

Title: US-09-516-728-1
perfect score: 0

Sequence: 1 QSRDTEVL 8

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum	DB	seq	length:	0
Maximum	DB	seq	length:	3

Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_032802:*

1:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT *
2:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT *
3:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT *
4:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT *
5:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT *
6:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT *
7:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT *
8:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT *
9:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT *
10:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT *
11:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT *
12:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT *
13:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT *
14:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT *
15:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT *
16:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT *
17:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT *
18:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT *
19:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT *
20:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT *
21:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT *
22:	/SDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	100.0	8	22	AAU03200	Sequence #1 for ep
2	8	100.0	1337	16	AAH85203	hudep-1. Homo sap
3	6	75.0	1911	22	ABH61038	Drosophila melano
4	5	62.5	14	21	AAV66911	T cell antigen rec
5	5	62.5	16	14	AAV51956	lipopolysaccharid
6	5	62.5	30	21	AAH03843	peptide Q0130 use
7	5	62.5	30	21	AAH03844	peptide R0130 use
8	5	62.5	50	22	AAE05149	Maize dof peptide
9	5	62.5	53	22	AAAG9826	ERA binding domain
10	5	62.5	54	22	AAU54869	Prpionibacterium
11	5	62.5	68	22	AAH78696	Human protein SEQ

12	5	62.5	68	22	AAM39020	Human polypeptide
13	5	62.5	72	13	AAR25119	Non- α , Non-B Hepat
14	5	62.5	90	21	AAB03841	Protein fragment #
15	5	62.5	90	21	AAB03842	Protein fragment #
16	5	62.5	93	22	AAU63362	Protonibacterium
17	5	62.5	93	22	AAU67333	Protonibacterium
18	5	62.5	105	22	AAU65387	Human brain expres
19	5	62.5	105	22	AAAT76402	Human bone marrow
20	5	62.5	105	22	AAAB3511	Peptide #10548 enc
21	5	62.5	116	21	AAU50927	Human fetal brain
22	5	62.5	118	22	AAU39232	Protonibacterium
23	5	62.5	118	22	AAU53773	Protonibacterium
24	5	62.5	121	21	AAAG01891	Human secreted pro
25	5	62.5	127	22	ABG18304	Novel human diagno
26	5	62.5	131	21	AAB57124	Novel prostate can
27	5	62.5	147	22	ABG16051	Novel human diagno
28	5	62.5	151	21	AAB25184	Eucalyptus grandis
29	5	62.5	178	21	AAU69981	Human N-acetyl tra
30	5	62.5	200	18	AAU55524	H. pylori ORF 29ep
31	5	62.5	216	22	AAU30554	Novel human secret
32	5	62.5	219	22	AAB80155	Corynebacterium g1
33	5	62.5	222	20	AAU37759	Amino acid sequenc
34	5	62.5	223	19	AAU98427	H. pylori GPO 398
35	5	62.5	227	18	AAU55386	H. pylori ORF 11ge
36	5	62.5	246	22	AAU72257	Human olfactory re
37	5	62.5	250	22	ABAB69076	Drosophila melanog
38	5	62.5	265	21	AAU94451	Human inflammation
39	5	62.5	271	21	AAU32239	Arabidopsis thalia
40	5	62.5	280	21	AAU32239	Arabidopsis thalia
41	5	62.5	284	21	AAU54774	Human secreted pro
42	5	62.5	286	21	AAU54774	Arabidopsis thalia
43	5	62.5	287	22	AAU32613	S. epidermidis ope
44	5	62.5	290	22	ABAB6450	Drosophila melanog
45	5	62.5	293	22	ABG08331	Novel human diagno

ALIGNMENTS

RESULT	1
AAU03200	
ID	AAU03200 standard; peptide; 8 AA
XY	

03-JAN-2002 (first entry)

Sequence #1 for epitope of ECRTP/DEP-1 ectodomain binding antibody

KM EORTC/DEE-1: endothelial cell receptor tyrosine phosphatase;
KM density enhanced phosphatase-1; anti-inflammatory; antiproliferatic;
KM antihemmatic; antidiabetic; antiatherosclerotic; cyostatic;
KM osteopathic; angiogenesis inhibitor; tumour; cancer.
XX

OS Mammalia.

PN WO200164750-A2

PD 07-SEP-2001.

PF 27-FEB-2001; 2001WO-US06178.

PR 01-MAR-2000; 2000US-0516728.

PA (UYVA-) UNIV VANDERBILT.
VY

PI Daniel TO, Takahashi T, Mernaugh R;
 YY

DR WPI; 2001-570681/64
YY

PT Novel antibody for modulating angiogenesis and endothelial cell
PT migration and proliferation, binds endothelial cell receptor tyrosine
PT phosphatase/density enhanced phosphatase-1 -

OY 1 OSDTE 6
 DB 450 dsrdte 455

RESULT 4

AA66911
 ID AAY66911 standard; peptide; 14 AA.

AC AAY66911;

DT 11-APR-2000 (first entry)

DE T cell antigen receptor Vbeta 17 chain peptide.

KM Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;

KW Vbeta chain; autoantigen; immunological tolerance.

OS Homo sapiens.

PN WO9963084-A1.

PD 09-DEC-1999.

PF 28-MAY-1999; 99WO-JP02814.

PR 29-MAY-1998; 98JP-0149855.

PR 14-OCT-1998; 98JP-0328761.

PA (TORI) TORII PHARM CO LTD.

PI Nishioka K, Yoshino S;

PI MPI; 2000-086978/07.

DR N-PSDB; AAZ96641.

PT T-cell antigen receptor V-beta chain CDR3 region sequences accumulated

PT in synovial membranes of rheumatoid arthritis patients -

PS Example 3; Page 103; 136pp; Japanese.

CC The invention relates to peptide sequences present in the synovial fluid
 CC and membranes of rheumatoid arthritis patients, arising from the CDR
 CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
 CC Compositions which contain autoantigenic peptides binding specifically
 CC to T-cells expressing receptors containing the peptide sequences, which
 CC include antigen-specific immunological tolerance to rheumatoid arthritis
 CC can be used for the treatment and prevention of rheumatoid arthritis.
 CC The invention can be used for the diagnosis, treatment and prevention
 CC of rheumatoid arthritis. Sequences AAY66771-958 represent peptides from
 CC the various Vbeta chains of T cell antigen receptor.

SO Sequence 14 AA;

Query Match 62.5%; Score 5; DB 21; Length 14;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SRDTE 6
 DB 6 srdte 10

RESULT 5

AA51956
 ID AAR51956 standard; Protein; 16 AA.

AC AAR51956;

DT 24-MAY-1994 (first entry)

DE Lipopolysaccharide induced protein (peptide fragment).

XX Macrophage; induced; lipo-polysaccharide; antitumour;
 KW antiinflammatory; trypanocidal agent; antibody; cell proliferation;
 KW activation; cytotoxicity.

OS Homo sapiens.

PN WO932437-A.

PD 11-NOV-1993.

PF 28-APR-1993; 93WO-EP01022.

PR 30-APR-1992; 92EP-0401231.

PA (INNO-) INNOCENETICS NV SA.

PI Devos K, Franssen L, Van De Voorde A, Van Heuverswyn H;

PI MPI; 1993-368796/46.

PT New polypeptide induced in macrophage(s) by lipo-polysaccharide -
 PT useful e.g. as antitumour, antiinflammatory or trypanocidal
 PT agent, also related nucleic acid, antibodies, anti-sense cpds.
 PT etc.

PS Claim 3; Page 67; 108pp; English.

CC The polypeptide induced in macrophages by lipopolysaccharide
 CC stimulates cell proliferation (esp. when costimulated with IL-4)
 CC promote activation, cytotoxicity, and mobilisation of LAK cells;
 CC promote recruitment of suppressive peritoneal exudate cells;
 CC promote generation of immunocompetent lymph node cells (LNC) and
 CC have trypanocidal and trypanolytic activity. The human and murine
 CC sequences are given in (AA051543-45), peptide fragments able to
 CC generate antibodies are given in (AAR51951-61)

SO Sequence 16 AA;

Query Match 62.5%; Score 5; DB 14; Length 16;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
 DB 10 dtevl 14

RESULT 6

AA03843
 ID AAB03843 standard; peptide; 30 AA.

AC AAB03843;

DT 20-OCT-2000 (first entry)

DE Peptide Q0130 used in TT virus antibody determination.

KW Serum type classification; TT virus; antibody; viral infection;
 KW identify; treatment.

OS TT virus.

PN JP2000135087-A.

PD 16-MAY-2000.

PF 29-OCT-1998; 98JP-0309208.

PR 29-OCT-1998; 98JP-0309208.

PA (SRLS-) SRL KK.

XX WPI; 2000-415430/36.
 DR
 XX Peptides for determination of anti-TT virus antibody and method for
 PT serum classification of TT virus using the peptides -
 XX
 PS Claim 4; Page 8; 12pp; Japanese.
 CC A method for serum type classification of TT virus (also known as
 CC hepatitis TT virus) has been identified. The method relies on the use of
 CC peptide fragments of the virus. The invention also relates to the use of
 CC TT virus peptides for anti-TT virus antibody determination. The anti-TT
 CC virus antibodies and the serum type classification method, can be used to
 CC screen TT virus, to determine its route of infection, and seroconversion.
 CC The classification of TT virus may lead to improved treatment of viral
 CC disease. The present sequence represents a fragment of TT virus protein
 CC used in the course of the invention.
 CC
 SQ Sequence 30 AA;

Query Match 62.5%; Score 5; DB 21; Length 30;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 RDETV 7
 |||||
 DB 26 rdtew 30

RESULT 7
 AAB03844
 ID AAB03844 standard; peptide; 30 AA.
 XX
 AC AAB03844;

DT 20-OCT-2000 (first entry)

DE Peptide R0130 used in TT virus antibody determination.

XX Serum type classification; TT virus; antibody; viral infection;
 KW identify; treatment.
 XX
 OS TT virus.

PN JP2000135087-A.

PD 16-MAY-2000.

PF 29-OCT-1998; 98JP-0309208.

PR 29-OCT-1998; 98JP-0309208.

PA (SRLS-) SRL KK.

DR WPI; 2000-415430/36.

PT Peptides for determination of anti-TT virus antibody and method for
 PT serum classification of TT virus using the peptides -
 XX
 PS Claim 6; Page 8; 12pp; Japanese.

CC A method for serum type classification of TT virus (also known as
 CC hepatitis TT virus) has been identified. The method relies on the use of
 CC peptide fragments of the virus. The invention also relates to the use of
 CC TT virus peptides for anti-TT virus antibody determination. The anti-TT
 CC virus antibodies and the serum type classification method, can be used to
 CC screen TT virus, to determine its route of infection, and seroconversion.
 CC The classification of TT virus may lead to improved treatment of viral
 CC disease. The present sequence represents a fragment of TT virus protein
 CC used in the course of the invention.
 CC
 SQ Sequence 30 AA;

Query Match 62.5%; Score 5; DB 21; Length 30;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 RDETV 7
 |||||
 DB 26 rdtew 30

RESULT 8
 AAE05149
 ID AAE05149 standard; peptide; 50 AA.
 XX
 AC AAE05149;

DT 12-SEP-2001 (first entry)

DE Maize DoF peptide domain ZMDOF2.

KW Maize; alpha-zein; Prolamin box binding factor peptide; PBF; DoF domain;
 KW transgenic plant; promoter; endosperm-specific protein; poultry feed;
 KW corn-soybean meal; cereal grain; oilseed crop; nutritional value; ZMDOF2.

OS Zea mays.

Key Location/Qualifiers

/note= "Residue Gly is present at this location in the
 sequence shown in sequence listing of the specification"

WO200149852-A1.

12-JUL-2001.

22-DEC-2000; 2000WO-US35185.

05-JAN-2000; 2000US-0174403.

(REGC) UNIV CALIFORNIA.

PI Schmidt RJ, Moose SP, Vicente-Carabajosa J;

DR WPI; 2001-441883/47.

XX Novel transgenic monocot plant, such as maize plant having increased
 XX methionine and/or lysine content in seeds, comprises recombinant
 PT prolamin box binding factor peptide gene -
 XX

PS Example 1; Fig 3; 48pp; English.

CC The invention relates to a transgenic monocot plant comprising an
 CC isolated DNA operably linked to a promoter, which is expressed to
 CC yield a prolamin box binding factor peptide (PBF). PBF then binds to
 CC promoter regions of 22-KD alpha-zein (prolamin seed storage proteins
 CC of maize are named zein) and 27-KD gamma-zein genes, so as to enhance
 CC gamma-zein production and lower alpha-zein production, so that
 CC methionine and lysine content of plant seed is increased over the content
 CC in native plant. PBF protein is a novel endosperm-specific cys2-cys2 zinc
 CC finger-type DNA binding protein of the DOF family. The transgenic monocot
 CC plant is a maize plant and expresses increased levels of methionine
 CC and/or lysine content in the seeds of the plant. The development of
 CC transgenic lines which supply higher levels of methionine reduces the
 CC need for methionine supplements for corn-soybean meal poultry feed and
 CC increased lysine content of either the cereal grains or the oilseed crops
 CC results in significant added nutritional value. The present is maize
 CC doF peptide domain ZMDOF2. This sequence contains a doF domain at the
 CC N-terminal end.
 CC
 SQ Sequence 50 AA;

Query Match 62.5%; Score 5; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSRDT 5
 |||||
 Db 5 gsrtd 9

RESULT 9

AG99826
 ID AAG99826 standard; Peptide; 53 AA.

AC AAG99826;

DE 27-SEP-2001 (first entry)

XX ERA binding domain polypeptide SEQ ID NO 268.

XX ERA binding domain; Escherichia coli; GTPase; antimicrobial;

KW antibacterial; antibiotic; pathogenesis; infection; vaccine;

XX peptide therapy.

OS Caenorhabditis elegans.

XX WO200153458-A2.

PD 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01786.

XX 18-JAN-2000; 2000US-0176870.

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

PI Lupas AN, Pearce KH;

XX WPI; 2001-476108/51.

XX New ERA binding domain polypeptides and polynucleotides encoding them,

PT useful as research reagents and materials for discovery of treatments

XX and diagnostics for diseases, or for genetic immunisation -

XX Claim 1; Page 37; 279pp; English.

XX The present invention relates to ERA binding domain polypeptides

CC (AAG99559-AAG9989 and AAM00010-AAM00021). The era gene in Escherichia

CC coli codes for an essential GTPase protein able to autophosphorylate at

CC serine and/or threonine residues. The protein has potential antimicrobial

CC and antibacterial activity and is useful in screening for antagonists,

CC agonists and for compounds with antibiotic activity. The proteins are

CC also useful in determining their role in pathogenesis of infection,

CC dysfunction and disease and could be used as part of a vaccine and/or

XX peptide therapy.

XX Sequence 53 AA;

XX Query Match 62.5%; Score 5; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
 |||||
 Db 4 dtevl 8

RESULT 10

AAU54869
 ID AAU54869 standard; Protein; 54 AA.

XX AAU54869;

XX 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #15765.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-199047P.

XX 02-JUN-2000; 2000US-208841P.

XX 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS39566.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

XX vaccinating against and diagnosing infections, especially useful for

XX treating acne vulgaris -

XX Example 1; SEQ ID NO 16064; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

CC polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by

CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 54 AA;

Query Match 62.5%; Score 5; DB 22; Length 54;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
 |||||
 Db 12 dtevl 16

RESULT 11

AAW78696
 ID AAW78696 standard; Protein; 68 AA.

XX AAW78696;

AC AAM78696;
XX
XX 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1358.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
PD 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX 20-JUN-2000; 2000US-0598075.
XX
XX 19-JUL-2000; 2000US-0620325.
XX
XX 01-SEP-2000; 2000US-0654936.
XX
XX 15-SEP-2000; 2000US-0663561.
XX
XX 20-OCT-2000; 2000US-0693325.
XX
XX 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX
XX N-PSDB: AAK51829.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 3607; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 68 AA;
SQ

Query Match 62.5%; Score 5; DB 22; Length 68;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSRDT 5
| | | | |
DB 2 gsrdt 6

RESULT 12
AAM39020
ID AAM39020 standard; Protein; 68 AA.
XX

AC AAM39020;
XX
XX 22-OCT-2001 (first entry)
XX
XX
DE Human polypeptide SEQ ID NO 2165.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX
XX 25-APR-2000; 2000US-0552317.
XX
XX 09-JUL-2000; 2000US-0598042.
XX
XX 19-JUL-2000; 2000US-0620312.
XX
XX 03-AUG-2000; 2000US-0653450.
XX
XX 14-SEP-2000; 2000US-0662191.
XX
XX 19-OCT-2000; 2000US-0693036.
XX
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wejhrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX
XX N-PSDB: AA158176.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Example 4; SEQ ID NO 2165; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAK42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX Sequence 68 AA;
SQ

Query Match 62.5%; Score 5; DB 22; Length 68;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSRDT 5
| | | | |
DB 2 gsrdt 6

```

RESULT 13
AAR25119
ID AAR25119 standard; Protein: 72 AA.
XX
AC AAR25119;
XX
DT 07-DEC-1992 (first entry)
XX
DE Non-A, Non-B Hepatitis Virus antigen #10.
XX
KM Antigen S29; NANBH; Hepatitis C; HCV; T064; T069; T06A; ELISA.
XX
OS Non-A Non-B Hepatitis Virus.
XX
PN W09209634-A.
XX
PD 11-JUN-1992.
XX
PE 29-NOV-1991; 91W0-JP0166Z.
XX
PR 29-NOV-1990; 90JP-0325434.
PR 29-NOV-1990; 90JP-0325435.
PR 16-JAN-1991; 91JP-0070231.
PR 19-APR-1991; 91JP-0179074.
PR 07-JUN-1991; 91JP-0232590.
XX
PA (TORA ) TORAY IND INC.
PI Arima T, Ida N, Kazami J, Sato A;
XX
DR WPI: 1992-217026/26.
DR N-PSDB; AAQ25749.
XX
PT New non-A non-B hepatitis virus antigen proteins - for highly
PT specific detection of hepatitis
XX
PS Claim 1; Page 49; 80pp; Japanese.
XX
CC This sequence is one of 12 claimed antigen sequences specific to
CC NANBH virus. The antigens can be used singly or in combination in
CC an ELISA diagnosis of hepatitis. See AAR24946 and AAR25110-R25121.
XX
SQ Sequence 72 AA;

Query Match 62.5%; Score 5; DB 13; Length 72;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DTEVL 8
Db 48 dtevl 52

```

```

RESULT 14
AAB03841
ID AAB03841 standard; protein: 90 AA.
XX
AC AAB03841;
XX
DT 20-OCT-2000 (first entry)
XX
DE Protein fragment #3 used in TT virus antibody determination.
XX
KM Serum type classification; TT virus; antibody; viral infection;
KM identify; treatment.
XX
OS TT virus.
XX
PN JP2000135087-A.
XX
PD 16-MAY-2000.
XX

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PF 29-OCT-1998; 98JP-0309208.
XX
PR 29-OCT-1998; 98JP-0309208.
XX
PA (SRLS-) SRL KK.
XX
DR WPI: 2000-415430/36.
XX
PT Peptides for determination of anti-TT virus antibody and method for
PT serum classification of TT virus using the peptides
XX
PS Claim 3; Page 7-8; 12pp; Japanese.
XX
CC A method for serum type classification of TT virus (also known as
CC hepatitis TT virus) has been identified. The method relies on the use of
CC peptide fragments of the virus. The invention also relates to the use of
CC TT virus peptides for anti-TT virus antibody determination. The anti-TT
CC virus antibodies and the serum type classification method, can be used to
CC screen TT virus, to determine its route of infection, and seroconversion.
CC The classification of TT virus may lead to improved treatment of viral
CC disease. The present sequence represents a fragment of TT virus protein
CC used in the course of the invention.
XX
SQ Sequence 90 AA;

Query Match 62.5%; Score 5; DB 21; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 RDTEV 7
Db 26 rdtev 30

```

```

RESULT 15
AAB03842
ID AAB03842 standard; protein: 90 AA.
XX
AC AAB03842;
XX
DT 20-OCT-2000 (first entry)
XX
DE Protein fragment #4 used in TT virus antibody determination.
XX
KM Serum type classification; TT virus; antibody; viral infection;
KM identify; treatment.
XX
OS TT virus.
XX
PN JP2000135087-A.
XX
PD 16-MAY-2000.
XX
PE 29-OCT-1998; 98JP-0309208.
XX
PR 29-OCT-1998; 98JP-0309208.
XX
PA (SRLS-) SRL KK.
XX
DR WPI: 2000-415430/36.
XX
PT Peptides for determination of anti-TT virus antibody and method for
PT serum classification of TT virus using the peptides
XX
PS Claim 3; Page 8; 12pp; Japanese.
XX
CC A method for serum type classification of TT virus (also known as
CC hepatitis TT virus) has been identified. The method relies on the use of
CC peptide fragments of the virus. The invention also relates to the use of
CC TT virus peptides for anti-TT virus antibody determination. The anti-TT
CC virus antibodies and the serum type classification method, can be used to
CC screen TT virus, to determine its route of infection, and seroconversion.
CC The classification of TT virus may lead to improved treatment of viral
CC disease. The present sequence represents a fragment of TT virus protein
CC used in the course of the invention.
XX

```

CC The classification of TT virus may lead to improved treatment of viral
CC disease. The present sequence represents a fragment of TT virus protein
CC used in the course of the invention.
XX
SQ Sequence 90 AA;

Query Match 62.5%; Score 5; DB 21; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 RDTEV 7
|||
Db 26 rdtev 30

Search completed: August 31, 2002, 12:20:01
Job time: 231 sec

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OM protein - protein search, using sw model

Run on: August 31, 2002, 12:19:30 ; Search time 24.94 Seconds
(without alignments)
55.492 Million cell updates/sec

Title: US-09-516-728-1
Perfect score: 8
Sequence: 1 QSRDTEVL 8

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	425	4	Q9NPR5	Q9NPR5 homo sapien
2	100.0	1337	4	Q15255	Q15255 homo sapien
3	87.5	654	11	Q9D0H7	Q9D0H7 mus musculu
4	75.0	152	2	Q9KY21	Q9KY21 streptomyc
5	75.0	524	2	Q9JGK2	Q9JGK2 klebsiella
6	75.0	576	10	Q9C923	Q9C923 arabidopsis
7	75.0	765	12	Q9JGS8	Q9JGS8 tt virus. p
8	75.0	765	12	Q9JGS5	Q9JGS5 tt virus. p
9	75.0	765	12	Q9JGS2	Q9JGS2 tt virus. p
10	75.0	1403	11	Q9QXG1	Q9QXG1 mus musculu
11	75.0	1911	5	Q9W4M7	Q9W4M7 drosophila
12	62.5	12	11	Q9WUX1	Q9WUX1 rectus norv
13	62.5	99	12	Q91704	Q91704 tt virus. o
14	62.5	99	12	Q91703	Q91703 tt virus. o
15	62.5	101	10	Q22031	Q22031 cyanidium c
16	62.5	105	13	Q91404	Q91404 xenopus lae

17	5	62.5	113	11	Q9D5W2	Q9D5W2 mus musculu
18	5	62.5	116	2	Q02327	Q02327 enterobacte
19	5	62.5	118	12	Q98515	Q98515 paramecium
20	5	62.5	119	2	Q85651	Q85651 streptomyc
21	5	62.5	143	4	Q9H5V1	Q9H5V1 homo sapien
22	5	62.5	143	11	Q9D5A6	Q9D5A6 mus musculu
23	5	62.5	146	12	Q9K527	Q9K527 mycobacteri
24	5	62.5	146	12	Q57208	Q57208 vaccinia vi
25	5	62.5	147	12	Q9JFA9	Q9JFA9 vaccinia vi
26	5	62.5	147	10	Q96390	Q96390 chlamydomon
27	5	62.5	160	4	Q9N0H6	Q9N0H6 homo sapien
28	5	62.5	166	16	Q9K6Y8	Q9K6Y8 bacillus ha
29	5	62.5	171	13	Q91881	Q91881 gallus gall
30	5	62.5	178	4	Q9H0Y4	Q9H0Y4 homo sapien
31	5	62.5	178	4	Q9Y6D2	Q9Y6D2 homo sapien
32	5	62.5	180	11	Q9D7H8	Q9D7H8 mus musculu
33	5	62.5	180	12	Q9J7I8	Q9J7I8 tt virus. o
34	5	62.5	180	16	Q9ZKR0	Q9ZKR0 helicobacte
35	5	62.5	183	16	Q985S5	Q985S5 rhizobium 1
36	5	62.5	187	16	Q9RXH1	Q9RXH1 deinococcus
37	5	62.5	188	11	Q9DBB2	Q9DBB2 mus musculu
38	5	62.5	192	4	Q9BSU2	Q9BSU2 homo sapien
39	5	62.5	192	12	Q9J7M2	Q9J7M2 tt virus. o
40	5	62.5	192	12	Q9J7M1	Q9J7M1 tt virus. o
41	5	62.5	201	5	Q94148	Q94148 caenorhabdi
42	5	62.5	205	15	Q72628	Q72628 human immun
43	5	62.5	206	4	Q96GV9	Q96GV9 homo sapien
44	5	62.5	209	5	Q18970	Q18970 caenorhabdi
45	5	62.5	212	2	Q9S239	Q9S239 streptomyc

ALIGNMENTS

RESULT 1
ID Q9NPR5 PRELIMINARY; PRT; 425 AA.
AC Q9NPR5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE PTPRJ, PROTEIN TYROSINE PHOSPHATASE RECEPTOR J, ETA (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Andreu N., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Aufray C., Ansoerge W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Poustka A., Lundeberg J.;
RT "The European IMAGE consortium for Integrated Molecular analysis of
human gene transcripts";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL359057; CAB94390.1; -;
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 2.
KW Receptor.
FT NON_TER
SQ SEQUENCE 425 AA; 45078 MW; BD1ACA5D345B7027 CRC64;

Query Match 100.0%; Score 8; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QSRDTEVL 8
DB 324 QSRDTEVL 331

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RESULT 2
ID 015255 PRELIMINARY; PRT: 1337 AA.
AC 015255;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95086212; PubMed=7994032;
RA Honda H.;
RT "Molecular cloning, characterization, and chromosomal localization of
RT a novel protein-tyrosine phosphatase, HPTeta."
RL Blood 84:4186-4194(1994).
DR EMBL: D37781; BAA07035.1;
DR HSSP: P18052; IYPO.
DR InterPro: IPR001385; Aldo_ket_red.
DR InterPro: IPR003961; FN_TT1.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_prot_phphatase.
DR Pfam: PF00041; fn3; 5.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PRTPHPTASE.
DR SMART: SM00060; FN3; 6.
DR SMART: SM00194; PTPc; 1.
DR PROSITE: PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
DR Hydroxylase; Signal; Transl. peptide.
KM SIGNAL 19 38 POTENTIAL.
FT TRANSIT 971 995
SQ SEQUENCE 1337 AA; 145802 MW; BA7EA3EE32961CBA CRC64;

Query Match 100.0%; Score 8; DB 4; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSRDTEVL 8
Db 324 QSRDTEVL 331

RESULT 3
ID 09D0H7 PRELIMINARY; PRT: 654 AA.
AC 09D0H7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE 2610016F07RIK PROTEIN.
GN POVI OR 2610016F07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=1121751;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saiko T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saiko R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyoko-Oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK011417; BAB27605.1;
DR MGD: MGI:1931352; Povi1
SQ SEQUENCE 654 AA; 72589 MW; FFD7521C2B2518BB CRC64;

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Query Match 87.5%; Score 7; DB 11; Length 654;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRDTEVL 8
Db 215 SRDTEVL 221

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RESULT 4
ID 09KY21 PRELIMINARY; PRT: 152 AA.
AC 09KY21;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PUTATIVE THIOL-SPECIFIC ANTIOXIDANT PROTEIN.
GN SCC8A.27C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
ON NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.,
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.,
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapate D., Elchner A., Cullum J.,
RA Kinsahl H., Hopwood D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
RT the 8 Mb streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL356892; CAB92845.1;
SQ SEQUENCE 152 AA; 16984 MW; 4A31560E7D853A0 CRC64;

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Query Match 75.0%; Score 6; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDETEVL 8
Db 63 RDETEVL 68

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RESULT 5
093GK2 PRELIMINARY; PRT; 524 AA.
ID 093GK2
AC 093GK2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MCEJ.
GN MCEJ.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_Taxid=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RYC492;
RX MEDLINE=99084959; PubMed=9864332;
RA Lagos R., Villanueva J.E., Monasterio O.;
RT "Identification and properties of the genes encoding microcin E492 and
RT its immunity protein.";
RL J. Bacteriol. 181:212-217(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RYC492;
RX MEDLINE=21537172; PubMed=11679081;
RA Lagos R., Baeza M., Corsini G., Hetr C., Strahsburger E.,
RA Castillo J.A., Vergara C., Monasterio O.;
RT "Structure, organization and characterization of the gene cluster
RT involved in the production of microcin E492, a channel-forming
RT bacteriocin.";
RL Mcl. Microbiol. 42:229-244(2001).
DR EMBL: AF063590; AL08403.1; -.
SQ SEQUENCE 524 AA; 59120 MW; 2F42260FBC80B923 CRC64;

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Query Match 75.0%; Score 6; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 3 RDTFVL 8
Db 42 RDTFVL 47

RESULT 6
09C923 PRELIMINARY; PRT; 576 AA.
ID 09C923;
AC 09C923;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE POTATIVE GTP-BINDING PROTEIN.
GN F14G24.25.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Becker U.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gall J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,

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RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shin P., Southwick A.M.,
RA Sun H., Tallon L.U., Tambunga G., Toriumi M.J., Town C.D.,
RA Ulterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL: AC019018; AA652287.1; -.
DR InterPro: IPR000765; GTP1_OBG.
DR InterPro: IPR002917; MMR_HSR1.
DR Pfam: PF01926; MMR_HSR1; 1.
DR PRINTS: PR00326; GTP1_OBG.
SQ SEQUENCE 576 AA; 65037 MW; E0CCAEAP979CBB0 CRC64;

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Query Match 75.0%; Score 6; DB 10; Length 576;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 QSRDTE 6
Db 367 QSRDTE 372

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RESULT 7
09UGS8 PRELIMINARY; PRT; 765 AA.
ID 09UGS8
AC 09UGS8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PORFL.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_Taxid=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20417334; PubMed=10963344;
RA Tanaka Y., Orito E., Ohno T., Nakano T., Hayashi K., Kato T.,
RA Mukaide M., Iida S., Mizokami M.;
RT "Identification of a 23kDa protein encoded by putative open-reading
RT frame 2 of TT virus (TTV) genotype 1 different from the other
RT genotypes.";
RL Arch. Virol. 145:1385-1398(2000).
DR EMBL: AB030487; BA990406.1; -.
DR InterPro: IPR004219; TT_ORF1.
DR Pfam: PF02956; TT_ORF1; 1.
SQ SEQUENCE 765 AA; 90225 MW; E845A26B69D9D707 CRC64;

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Query Match 75.0%; Score 6; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 3 RDTFVL 8
Db 663 RDTFVL 668

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RESULT 8
09UGS5 PRELIMINARY; PRT; 765 AA.
ID 09UGS5
AC 09UGS5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PORFL.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_Taxid=68887;
RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=2041734; PubMed=10963344;
RA Tanaka Y., Orito E., Ohno T., Nakano T., Hayashi K., Kato T.,
RT Mukide M., Iida S., Mizokami M.;
RT "Identification of a 23kDa protein encoded by putative open reading
RT frame 2 of TT virus (TTV) genotype 1 different from the other
RT genotypes";
RL Arch. Virol. 145:1385-1398(2000).
DR EMBL; AB030488; BAA90409.1; -.
DR InterPro: IPR004219; TT_ORF1.
DR Pfam: PF02956; TT_ORF1; 1.
SQ SEQUENCE 765 AA; 90275 MW; 707029EB45829B5F CRC64;

Query Match 75.0%; Score 6; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RDEVL 8
|||||
Db 663 RDEVL 668

RESULT 9
QJUGS2 PRELIMINARY; PRT; 765 AA.
AC QJUGS2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE POR1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2041734; PubMed=10963344;
RA Tanaka Y., Orito E., Ohno T., Nakano T., Hayashi K., Kato T.,
RA Mukide M., Iida S., Mizokami M.;
RT "Identification of a 23kDa protein encoded by putative open reading
RT frame 2 of TT virus (TTV) genotype 1 different from the other
RT genotypes";
RL Arch. Virol. 145:1385-1398(2000).
DR EMBL; AB030488; BAA90412.1; -.
DR InterPro: IPR004219; TT_ORF1.
DR Pfam: PF02956; TT_ORF1; 1.
SQ SEQUENCE 765 AA; 90401 MW; 2E04F82EC74CF86A CRC64;

Query Match 75.0%; Score 6; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RDEVL 8
|||||
Db 663 RDEVL 668

RESULT 10
Q90XG1 PRELIMINARY; PRT; 1403 AA.
AC Q90XG1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MUCIN MUC4 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartman A.E., Shekels L.L., Anway R.E., Gipson I.K., Moccia R.,

RA Ho S.B.;
RT "Identification and structure of a Mouse Homolog to the Human MUC4
RT Gene";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF218265; AAF23818.1; -.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003886; Nidogen_ext.
DR InterPro: IPR001846; vwd.
DR Pfam: PF00094; vwd; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00539; NIDO; 1.
DR SMART: SM00216; vwd; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR NON_TER 1
SQ SEQUENCE 1403 AA; 154669 MW; 0A51AFB7ED52EA7C CRC64;

Query Match 75.0%; Score 6; DB 11; Length 1403;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RDEVL 8
|||||
Db 768 RDEVL 773

RESULT 11
Q9M4M7 PRELIMINARY; PRT; 1911 AA.
AC Q9M4M7; 097423; 097424;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE CG4857 PROTEIN.
GN CG4857 OR EG-EG0007.4 OR EG-EG0007.12.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins M.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burdick K.C., Busam D.A., Butler H., Cadieu E., Gentler A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Part V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao S., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RX MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Gallibert F., Borkova D.,
 RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
 RA Mocollet J., Peter A., Schoettler P., Werner M., Moutkioti F.,
 RA Bellert N., Dove G., Schaefer U., Jaekle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlamsiou A., Henderson N.S.,
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 RT melanogaster.";
 RL Science 287:2220-2222(2000).
 DR EMBL: AE003430; AAF45924.1; -.
 DR EMBL: AL033125; CAA21827.1; ALT_SEQ.
 DR EMBL: AL033125; CAA21828.1; ALT_SEQ.
 DR FlyBase: FBgn026083; CG4857.
 RW Hypothetical protein.
 SQ SEQUENCE 1911 AA; 199630 MW; 78EBE281C9EFE93F CRC64;

Query Match 75.0%; Score 6; DB 5; Length 1911;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 450 QSRDTE 455
 QY 1 QSRDTE 6
 ID 111111
 AC Q9WUX1 PRELIMINARY; PRT; 12 AA.
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE APOBEC-1 PROTEIN (FRAGMENT).
 GN APOBEC-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98335789; PubMed=9672068;
 RA Greene J., Axelos D., Welker S., Schipper M., Gieten H.;
 RT "Distinct promoters induce APOBEC-1 expression in rat liver and
 RT intestine.";
 RL Arterioscler. Thromb. Vasc. Biol. 18:1079-1092(1998).
 DR EMBL: AJ006695; CAB44439.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1357 MW; 70FB1679699325BB CRC64;

Query Match 62.5%; Score 5; DB 11; Length 12;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRDTE 6
 ID 11111
 Db 1 SRDTE 5
 RESULT 13
 Q91704
 ID Q91704 PRELIMINARY; PRT; 99 AA.
 AC Q91704;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DE ORF1 (FRAGMENT).
 OS TT virus.
 CC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TVSD4;
 RA Yu J.G., Shang Q.H., Ren H.;
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF416141; AAL15657.1; -.
 DR EMBL: AF416141; AAL15657.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 99 AA; 11477 MW; 4FBAC10D643C1404 CRC64;

Query Match 62.5%; Score 5; DB 12; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 32 RDTEV 36
 QY 3 RDTEV 7
 ID 11111
 AC Q91703 PRELIMINARY; PRT; 99 AA.
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE ORF1 (FRAGMENT).
 GN TT virus.
 OS Viruses; ssDNA viruses; unclassified ssDNA viruses.
 CC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TVSD5;
 RA Yu J.G., Shang Q.H., Ren H.;
 RT "Transfusion transmitted virus (TTV) sequence.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF416142; AAL15658.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 99 AA; 11476 MW; C5AAC10D643C1AE4 CRC64;

Query Match 62.5%; Score 5; DB 12; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 32 RDTEV 36
 QY 3 RDTEV 7
 ID 11111
 Db 32 RDTEV 36
 RESULT 15
 O22031
 ID O22031 PRELIMINARY; PRT; 101 AA.

AC 022031;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE THIOREDOXIN M.
GN TRXM.
OS Cyanidium caldarium.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
OX NCBI_TaxID-2771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RK-1;
RA Ohta N.;
RL J. Plant Res. 110:235-245(1997).
DR EMBL: D63676; BAA22827.1; -.
DR HSSP: P00274; 1T7P.
DR InterPro: IPR000063; ThioRed.
DR Pfam: PF00085; ThioRed; 1.
DR PRINTS: PR00421; THIOREDOXIN.
DR PROSITE: PS00194; THIOREDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 101 AA; 11476 MW; 7678E87CFB82B098 CRC64;

Query Match 62.5%; Score 5; DB 10; Length 101;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 DTEVL 8
|||||
DB 9 DTEVL 13

Search completed: August 31, 2002, 12:23:05
Job time: 215 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 31, 2002, 12:11:34 ; Search time 30 Seconds
(without alignments)
29,620 Million cell updates/sec

Title: US-09-516-728-1

Perfect score: 38

Sequence: 1 OSRDREV.L 8

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	8	22	AAU03200
2	38	100.0	1337	16	AA85203
3	31	81.6	121	21	AA01891
4	31	81.6	162	21	AA014427
5	31	81.6	162	21	AA038115
6	31	81.6	180	21	AA014426
7	31	81.6	180	21	AA038114
8	31	81.6	252	21	AA014425
9	31	81.6	252	21	AA038113
10	31	81.6	543	22	AB864811
11	31	81.6	549	22	AB850168

12	30	78.9	385	21	AA054590	zea mays protein f
13	30	78.9	395	21	AA054588	zea mays protein f
14	30	78.9	422	21	AA054589	zea mays protein f
15	30	78.9	431	22	AA042384	Human polypeptide
16	30	78.9	513	22	AA040282	Human polypeptide
17	30	78.9	513	22	AA031194	Human protein sequ
18	30	78.9	513	22	AA068510	Human GTP-binding
19	30	78.9	525	22	AA042068	Human polypeptide
20	30	78.9	1911	22	AB061038	Drosophila melanog
21	29	76.3	234	19	AA061015	Streptococcus pneu
22	29	76.3	361	22	AB068291	Drosophila melanog
23	29	76.3	1033	22	AA001097	CPE 100 protein se
24	29	76.3	1042	22	AA037752	Streptococcus pneu
25	29	76.3	1042	22	AA097699	Streptococcus pneu
26	29	76.3	1872	22	AA079160	Human protein SEQ
27	29	76.3	2443	22	AB060521	Drosophila melanog
28	28	73.7	75	18	AA026420	Swinepox virus Hin
29	28	73.7	75	22	AA068241	Protein encoded by
30	28	73.7	109	22	AB027651	Human peptide #302
31	28	73.7	109	22	AB032821	Protein #302 encod
32	28	73.7	109	22	AB018303	Human brain expres
33	28	73.7	109	22	AA053628	Human bone marrow
34	28	73.7	109	22	AA066007	Human brain expres
35	28	73.7	109	22	AA013876	Peptide #310 encod
36	28	73.7	109	22	AA026283	Peptide #320 encod
37	28	73.7	109	22	AA001619	Peptide #301 encod
38	28	73.7	134	22	AA005568	Human polypeptide
39	28	73.7	162	22	AB011474	Novel human diagno
40	28	73.7	165	21	AA040093	Arabidopsis thalia
41	28	73.7	168	22	AA029724	Novel human secret
42	28	73.7	183	21	AA040092	Arabidopsis thalia
43	28	73.7	255	21	AA040091	Arabidopsis thalia
44	28	73.7	287	22	AA092613	S. epidemidis ope
45	28	73.7	448	21	AA012584	Naphthalene dioxyg

ALIGNMENTS

RESULT 1

AAU03200

ID AAU03200 standard; peptide; 8 AA.

XX

AAU03200;

XX

03-JAN-2002 (first entry)

DE Sequence #1 for epitope of ECRTp/DEP-1 ectodomain binding antibody.

XX

ECRTp/DEP-1; endothelial cell receptor tyrosine phosphatase;

KW density enhanced phosphatase-1; anti-inflammatory; antiproliferative;

KW antineoplastic; antidiabetic; antithrombotic; antitumor; antiproliferative;

XX osteopetrotic; angiogenesis inhibitor; tumor; cancer.

XX

OS Mammalia.

XX

WO200164750-A2.

PN

07-SEP-2001.

XX

27-FEB-2001; 2001WO-US06178.

XX

01-MAR-2000; 2000US-0516728.

PR

(UYVA-) UNIV VANDERBILT.

PA

Daniel TO, Takahashi T, Mernaugh R;

XX

WPI; 2001-570681/64.

DR

Novel antibody for modulating angiogenesis and endothelial cell

PT migration and proliferation; binds endothelial cell receptor tyrosine

PT phosphatase/density enhanced phosphatase-1

XX Example 4: Page 82; 110pp; English.
 CC The invention describes a novel purified antibody (or its fragment or
 CC derivative) which preferentially binds an endothelial cell receptor
 CC tyrosine phosphatase/density enhanced phosphatase-1 (ECRTP/DEP-1). The
 CC antibody has antiinflammatory, antiproliferative, antithrombotic,
 CC antidiabetic, antiatherosclerotic, cyostatic and osteopathic activities
 CC and may be an ECRTP/DEP-1 modulator, ECRTP/DEP-1 dimerisation promoter or
 CC antagonist and angiogenesis inhibitor. The purified antibody blocks
 CC endothelial migration and proliferation and inhibits angiogenesis in
 CC disorders such as inflammatory disorders including immune and non-immune
 CC inflammation, chronic articular rheumatism and psoriasis, disorders
 CC associated with inappropriate invasion of vessels such as diabetic
 CC retinopathy, neovascular glaucoma, capillary proliferation in
 CC atherosclerotic plaques, osteoporosis and cancer associated disorders
 CC such as solid tumours, solid tumour metastases, angiofibromas,
 CC retrolental fibroplasia, hemangiomas, Kaposi's sarcoma and similar
 CC cancers. This sequence is peptide sequence #1 for epitope ECRTP/DEP-1
 CC ectodomain binding antibody used to modulate angiogenesis, described in
 CC the method of the invention.
 CC Note: This sequence for ECRTP/DEP-1 epitope, given in example 4, differs
 CC from that given in claim 3 (AAU08802).
 CC
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 38; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QSRDTEVL 8
 DB 1 gsrdevl 8
 RESULT 2
 AAR85203
 ID AAR85203 standard; Protein; 1337 AA.
 AC AAR85203;
 XX
 XX 12-FEB-1996 (first entry)
 DE huDEP-1.
 DE huDEP-1.
 KM Density enhanced Type III receptor-like protein tyrosine phosphatase;
 KM huDEP-1.
 OS Homo sapiens.
 OS
 PM W09530008-A1.
 PM
 PD 09-NOV-1995.
 PD
 PF 03-MAY-1995; 95WO-US05512.
 PF
 PR 03-MAY-1994; 94US-0237940.
 PR
 PA (COLD-) COLD SPRING HARBOR LAB.
 PA
 PI Oestman A, Tonks NK;
 PI
 XX WPI: 1995-393079/50.
 DR N-PSDB: AAT06027.
 DR
 XX New density enhanced protein tyrosine phosphatase - used to develop
 PT prods. to modify transcription, translation and/or activity of
 PT tyrosine phosphatase(s).
 PT
 XX Claim 4: Page 34-38; 51pp; English.
 PS A cDNA clone was obtd. (see AAT06027) from a HeLa cell cDNA library
 CC

CC that encoded a novel density-enhanced Type III receptor-like PTP,
 CC designated huDEP-1 (AAR85203). huDEP-1 is useful for the study of PTPs
 CC and for the development of therapeutic or prophylactic cpds. e.g. for
 CC prevention of abnormal or malignant cell growth.
 CC
 SQ Sequence 1337 AA;
 Query Match 100.0%; Score 38; DB 16; Length 1337;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QSRDTEVL 8
 DB 324 gsrdevl 331
 RESULT 3
 AAG01891
 ID AAG01891 standard; Protein; 121 AA.
 AC AAG01891;
 XX
 XX 06-OCT-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 5972.
 DE
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 OS
 PM EPI033401-A2.
 PM
 PD 06-SEP-2000.
 PD
 PF 21-FEB-2000; 2000EP-0200610.
 PF
 PR 26-FEB-1999; 99US-0122487.
 PR
 PA (GEST) GENSET.
 PA
 PI Dumas Mline Edwards J, Duclert A, Giordano J;
 PI
 XX WPI: 2000-500381/45.
 DR N-PSDB: AAC01897.
 DR
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 PT
 XX Claim 13; SEQ ID 5972; 71pp + CD-ROM; English.
 PS
 XX The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 CC
 SQ Sequence 121 AA;
 Query Match 81.6%; Score 31; DB 21; Length 121;
 Best Local Similarity 75.0%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSRDTEVL 8
||||:|
Db 113 qsrdrp1 120

RESULT 4
AAG14427
ID AAG14427 standard; Protein; 162 AA.
XX
AC AAG14427;
XX
DE 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SPQ ID NO: 14285.
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hydrolisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
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Query Match Best Local Similarity 81.6%; Score 31; DB 21; Length 162;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 152 gardsdvl 159

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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XX
DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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PD 06-SEP-2000.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 81.6%; Score 31; DB 21; Length 180;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSRDTEVL 8
Db 170 qsrdsdvl 177

RESULT 7
AAG38114
ID AAG38114 standard; Protein: 180 AA.
XX

AC AAG38114;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 46971.

XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

XX Arabidopsis thaliana.
OS

XX Ep1033405-A2.
XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
EF XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 01-JUL-1999; 99US-0141842.
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PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
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PR 23-AUG-1999; 99US-0149902.
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PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.

PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
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PR 23-SEP-1999; 99US-0155486.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 12-OCT-1999; 99US-0158365.
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PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 81.6%; Score 31; DB 21; Length 180;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OSRDTEVL 8
Db 170 gardsdvl 177

RESULT 8
ID AGG14425 standard; Protein; 252 AA.

AC AGG14425;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SFG ID NO: 14283.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0137753.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 81.6%; Score 31; DB 21; Length 252;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSRDREVL 8
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Db 242 gardscvl 249

RESULT 9
AAG38113
ID AAG38113 standard; Protein; 252 AA.
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AC AAG38113;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46970.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
OS
PM EPI033405-A2.
PM
PD 06-SEP-2000.
PD
XX
PF 25-FEB-2000; 2000EP-0301439.
PF
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 29-OCT-1999; 99US-0162142.

Query Match 81.6%; Score 31; DB 21; Length 252;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 OSRDREVL 8
Db 242 gstdsavl 249

RESULT 10
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ID ABB64811 standard; Protein: 543 AA.
XX
AC ABB64811;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 21225.
XX
KW Drosophila melanogaster polypeptide SEQ ID NO 21225.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PE 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
DR N-PSDB; ABL08914.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 21225; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX

SQ Sequence 543 AA;

Query Match 81.6%; Score 31; DB 22; Length 543;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSRDREV 7
|||||:
Db 429 gsrtdtv 435

RESULT 11
ABB50168
ID ABB50168 standard; Protein; 549 AA.

XX ABB50168;

DT 05-FEB-2002 (first entry)

XX Human transcription factor TRFX-19.

XX Human; transcription factor; TRFX; cell proliferative disease;

KW autoimmune disease; inflammation; neurological disease;

KW developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;

KW neuroprotective; antiinflammatory; gene therapy.

XX Homo sapiens.

XX WO200172777-A2.

XX 04-OCT-2001.

XX 13-MAR-2001; 2001WO-US08117.

XX 13-MAR-2000; 2000US-0188986.

XX (INCYTE) INCYTE GENOMICS INC.

XX Hillman JL, Baughn MR, Yue H, Lal P, Lu DM, Patterson C;

PI Azimzai Y, Bandman O, Tang YT, Mathur P, Shah P, Au-Young J;

PI Reddy R;

XX WPI: 2001-570896/64.

DR N-PSDB; ABA82992.

XX Novel transcription factor polypeptides, used to treat diseases
PT associated with altered activity and expression of TRFX, and to screen
PT for agents capable of modulating its activity -
XX

PS Claim 1; Pages 161-162; 327pp; English.

CC The present sequence is the protein sequence for a human transcription
CC factor. The transcription factor and its coding sequence are useful in
CC the diagnosis, treatment and prevention of diseases associated with
CC altered expression of the transcription factor e.g. cell proliferative,
CC autoimmune/inflammatory, neurological and developmental disorders. A
CC number of specific disorders/diseases are given in the specification,
CC including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,
CC allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic

CC dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,
CC Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis,
CC psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative
CC colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, stroke, and viral, bacterial, fungal and protozoal infections.
XX

SQ Sequence 549 AA;

Query Match 81.6%; Score 31; DB 22; Length 549;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 OSRDREV 8
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Db 113 gsrtdp11 120

RESULT 12
AAG54590
ID AAG54590 standard; Protein; 385 AA.

XX AAG54590;

DT 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 69621.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 14-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999;	99US-0136392.
PR 28-MAY-1999;	99US-0136782.
PR 01-JUN-1999;	99US-0137222.
PR 03-JUN-1999;	99US-0137528.
PR 04-JUN-1999;	99US-0137502.
PR 07-JUN-1999;	99US-0137724.
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PR 10-JUN-1999;	99US-0138540.
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PR 16-JUN-1999;	99US-0139452.
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PR 04-AUG-1999;	99US-0147204.
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PR 23-AUG-1999;	99US-0149930.
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PR 31-AUG-1999;	99US-0151303.
PR 01-SEP-1999;	99US-0151438.
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PR 15-SEP-1999;	99US-0153758.
PR 16-SEP-1999;	99US-0154018.
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PR 28-OCT-1999;	99US-0161992.
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PR 29-OCT-1999; 99US-0162142.
Query Match 78.9%; Score 30; DB 21; Length 385;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSRDREV 7
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Db 95 gtrdel 101
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AAG54589
ID AAG54589 standard; Protein; 395 AA.
XX AAG54589;
AC AAG54589;
XX 18-OCT-2000 (first entry)
DT 18-OCT-2000 (first entry)
XX
XX Zea mays protein fragment SEQ ID NO: 69620.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
XX Zea mays subsp. mays.
XX
XX EPI033405-A2.
PN
XX 06-SEP-2000.
PD
XX 25-FEB-2000; 2000EP-0301439.
PE
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 01-JUL-1999; 99US-0142154.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 04-OCT-1999; 99US-0157117.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 78.9%; Score 30; DB 21; Length 395;
Best Local Similarity 71.4%; Pred. No. 3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0;

OY 1 OSRDTEV 7

Db 105 gtrdtei 111

RESULT 14

AAG54588
ID AAG54588 standard; Protein; 422 AA.

XX AAG54588;

DT 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 69619.

XX Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence; corn.

XX Zea mays subsp. mays.

OS EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

PF 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0128845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

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PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

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PR 04-JUN-1999; 99US-0137724.

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PR 08-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

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PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

XX AAM42384;
 AC 22-OCT-2001 (first entry)
 XX
 DT Human polypeptide SEQ ID NO 117.
 DE
 XX Human: nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antisticking; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatoprotective; cerebroprotective; antiinflammatory;
 KW antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX WO200155449-A1.
 XX
 PD 02-AUG-2001.
 XX
 PE 17-JAN-2001; 2001WO-US01346.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUL-2000; 2000US-0216880.
 PR 14-JUL-2000; 2000US-0218290.
 PR 14-AUG-2000; 2000US-0225447.
 PR 01-SEP-2000; 2000US-0229343.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0231243.
 PR 25-SEP-2000; 2000US-0234997.
 PR 29-SEP-2000; 2000US-0236367.
 PR 13-OCT-2000; 2000US-0239937.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246528.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249214.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-476225/51.
 DR N-PSDB; AAI62789.
 XX
 XX Novel plasma membrane associated proteins useful for diagnosing,
 PT treating, preventing and/or prognosing disorders related to the
 PT proteins, including cancer, immune response and neuronal disorders -
 XX
 PS Claim 11; SEQ ID NO 117; 532pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (AAI62752-AAI62961) and proteins
 CC (AAM42347-AAM42415) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 431 AA;

Query Match 78.9%; Score 30; DB 22; Length 431;
 Best Local Similarity 85.7%; Pred. No. 3.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SRRPEVL 8
 Db 299 srrdtml 305

Search completed: August 31, 2002, 12:15:26
 Job time: 232 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 31, 2002, 12:13:24 ; Search time 12.97 Seconds
(without alignments)
15.066 Million cell updates/sec

Title: US-09-516-728-1

Perfect score: 38

Sequence: 1 QSRDREVL 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2.6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2.6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2.6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2.6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2.6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2.6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	1337	3	US-08-854-585-2
2	38	100.0	1337	5	PCT-US95-05512-2
3	29	76.3	1042	4	US-09-387-695-2
4	29	76.3	1839	2	US-09-172-977-4
5	28	73.7	75	1	US-08-307-499-21
6	28	73.7	75	4	US-09-299-268-21
7	27	71.1	357	1	US-08-356-405-2
8	27	71.1	371	4	US-08-806-263-2
9	27	71.1	380	4	US-08-969-815-4
10	27	71.1	380	4	US-09-120-025-4
11	27	71.1	432	1	US-08-167-919A-11
12	27	71.1	432	3	US-08-715-106-11
13	27	71.1	465	4	US-09-150-440-1
14	27	71.1	760	4	US-08-914-999-12
15	27	71.1	768	4	US-08-914-999-10
16	27	71.1	898	3	US-08-863-102-1
17	27	71.1	898	3	US-08-863-102-4
18	27	71.1	907	3	US-08-863-102-2
19	27	71.1	1100	1	US-08-357-598-11
20	27	71.1	1100	2	US-09-003-289-11
21	27	71.1	1100	5	PCT-US95-16435-11
22	26	68.4	139	4	US-08-858-207A-429
23	26	68.4	165	3	US-08-844-154-4
24	26	68.4	165	3	US-09-126-192A-4
25	26	68.4	200	2	US-09-031-485-12
26	26	68.4	200	2	US-08-847-429A-12
27	26	68.4	200	3	US-09-065-474-12

28	26	68.4	201	1	US-07-929-580B-5	Sequence 5, Appli
29	26	68.4	223	1	US-07-708-885B-3	Sequence 3, Appli
30	26	68.4	223	1	US-07-714-386-3	Sequence 3, Appli
31	26	68.4	223	1	US-07-708-888A-3	Sequence 3, Appli
32	26	68.4	422	3	US-09-065-474-142	Sequence 142, App
33	26	68.4	434	2	US-08-844-154-2	Sequence 2, Appli
34	26	68.4	434	3	US-09-126-192A-2	Sequence 2, Appli
35	26	68.4	447	2	US-08-902-585-2	Sequence 2, Appli
36	26	68.4	650	1	US-08-121-713D-60	Sequence 60, Appl
37	26	68.4	650	1	US-08-835-268-60	Sequence 60, Appl
38	26	68.4	650	2	US-09-060-682-60	Sequence 60, Appl
39	26	68.4	650	3	US-08-833-391-60	Sequence 60, Appl
40	26	68.4	650	4	US-09-060-610-60	Sequence 60, Appl
41	26	68.4	650	5	PCT-US94-10151A-60	Sequence 60, Appl
42	26	68.4	1462	3	US-07-792-600-31	Sequence 31, Appl
43	26	68.4	1462	3	US-09-157-021-31	Sequence 31, Appl
44	26	68.4	1462	3	US-09-156-842-31	Sequence 31, Appl
45	26	68.4	1745	2	US-09-031-485-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-854-585-2
; Sequence 2, Application US/08854585
; Patent No. 6114140
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K. and stman, Arne
; TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,585
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,940
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-854-585-2

Query Match 100.0%; Score 38; DB 3; Length 1337;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSRDREVL 8
DB 324 QSRDREVL 331

RESULT 2
PCT-US95-05512-2
; Sequence 2, Application PC/TUS9505512
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K. and Stuman, Arne
; TITLE OF INVENTION: Density Enhanced Protein Tyrosine
; TITLE OF INVENTION: Phosphatase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05512
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27866/31954
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-05512-2

Query Match 100.0%; Score 38; DB 5; Length 1337;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSRDREVL 8
Db 324 QSRDREVL 331

RESULT 3
US-09-387-695-2
; Sequence 2, Application US/09387695
; Patent No. 6280990
; GENERAL INFORMATION:
; APPLICANT: May, Earl
; APPLICANT: Van Horn, Stephanie
; APPLICANT: Warren, Patrick V.
; APPLICANT: Warren, Richard L.
; TITLE OF INVENTION: dnae
; FILE REFERENCE: GM10237
; CURRENT APPLICATION NUMBER: US/09/387,695
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1042
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-387-695-2

Query Match 76.3%; Score 29; DB 4; Length 1042;

Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QSRDREVL 8
Db 169 ESRDREVL 176

RESULT 4
US-09-172-977-4
; Sequence 4, Application US/09172977
; Patent No. 5989663
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
; FILE REFERENCE: PF-0615 US
; CURRENT APPLICATION NUMBER: US/09/172,977
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1839
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: g29491
US-09-172-977-4

Query Match 76.3%; Score 29; DB 2; Length 1839;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSRDREVL 8
Db 136 RSRDREVL 1343

RESULT 5
US-08-307-499-21
; Sequence 21, Application US/08307499
; Patent No. 5651972
; GENERAL INFORMATION:
; APPLICANT: Meyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,499
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630

FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanhik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-499-21

Query Match 73.7%; Score 28; DB 1; Length 75;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDTFVL 8
||||:|
Db 58 RDTFEL 63

RESULT 6

US-09-299-268-21
Sequence 21, Application US/09299268
Patent No. 621/782
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanhik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/901,127
FILING DATE:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanhik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-268-21

Query Match 73.7%; Score 28; DB 4; Length 75;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RDTFVL 8
||||:|
Db 58 RDTFEL 63

RESULT 7

US-08-356-405-2
Sequence 2, Application US/08356405
Patent No. 5807691
GENERAL INFORMATION:
APPLICANT: Amlaky, No. 5807691rdine
APPLICANT: Boschert, Ursula
APPLICANT: Hen, Rene
APPLICANT: Plassat, Jean-Luc
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5a), Nucleic Acids Coding for these
TITLE OF INVENTION: Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,405
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: EX92004-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-405-2

Query Match 71.1%; Score 27; DB 1; Length 357;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QSRDTEVL 8
:|||||
DB 22 SRDTEVL 29

RESULT 8

US-08-806-263-2
; Sequence 2, Application US/08806263
; Patent No. 6221627
; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: cDNA Clone HDPH130 That Encodes
; TITLE OF INVENTION: A No. 6221627el Human 7-Transmembrane Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806,263
; FILING DATE: 24-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-806-263-2

Query Match 71.1%; Score 27; DB 4; Length 371;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 SRDTEVL 8
:|||||
DB 332 SRDTEVL 338

RESULT 9

US-08-969-815-4
; Sequence 4, Application US/08969815
; Patent No. 6207412
; GENERAL INFORMATION:
; APPLICANT: Wille, Owen N.
; APPLICANT: Weng, Zhigang

;; TITLE OF INVENTION: IDENTIFICATION OF A G PROTEIN-COUPLED
;; TITLE OF INVENTION: RECEPTOR TRANSCRIPTIONALLY REGULATED BY PROTEIN
;; TITLE OF INVENTION: TYROSINE KINASE SIGNALING IN HEMATOPOIETIC CELLS
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Knobbe, Martens, Olson & Bear
;; STREET: 620 Newport Center Drive, 16th Floor
;; CITY: Newport Beach
;; STATE: CA
;; COUNTRY: U.S.A.
;; ZIP: 92660
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/969,815
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bartfeld, Neil S
;; REGISTRATION NUMBER: 39,901
;; REFERENCE/DOCKET NUMBER: UCLAO15.001A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-235-8550
;; TELEFAX: 619-235-0176
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 380 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
;; US-08-969-815-4

Query Match 71.1%; Score 27; DB 4; Length 380;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 SRDTEVL 8
:|||||
DB 341 SRDTEVL 347

RESULT 10
US-09-120-025-4
; Sequence 4, Application US/09120025
; Patent No. 6214562
; GENERAL INFORMATION:
; APPLICANT: Weng, Zhigang
; APPLICANT: Wille, Owen N.
; TITLE OF INVENTION: TRANSCRIPTIONALLY REGULATED G PROTEIN-COUPLED
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/120, 025
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/969, 815
;; FILING DATE: 13-NOV-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bartfeld, Neil S
;; REGISTRATION NUMBER: 39,901
;; REFERENCE/DOCKET NUMBER: UCLAD15, 001CPI
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-235-8550
;; TELEFAX: 619-235-0176
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 380 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: Internal
;; US-09-120-025-4

Query Match 71.1%; Score 27; DB 4; Length 380;
Best Local Similarity 85.7%; Pred. NO. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 SRDTEVL 8
Db 341 SRDTEVL 347

RESULT 11
US-08-167-919A-11
; Sequence 11, Application US/08167919A
; Patent No. 5674691
; GENERAL INFORMATION:
; APPLICANT: Boyd, Andrew W.
; APPLICANT: Simpson, Richard J.
; APPLICANT: Wicks, Ian
; APPLICANT: Ward, Larry D.
; APPLICANT: Wilkinson, David
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167, 919A
; FILING DATE: 18-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK6841 (AU)
; FILING DATE: 21-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK9992 (AU)
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00294
; FILING DATE: 19-JUN-1992

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Digilio, Frank S.
;; REGISTRATION NUMBER: 31,346
;; REFERENCE/DOCKET NUMBER: 9159
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; TELEX: 230 901 SANS UR
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 432 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-167-919A-11

Query Match 71.1%; Score 27; DB 1; Length 432;
Best Local Similarity 85.7%; Pred. NO. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 SRDTEVL 8
Db 177 SRDTEVL 183

RESULT 12
US-08-715-106-11
; Sequence 11, Application US/08715106
; Patent No. 6020306
; GENERAL INFORMATION:
; APPLICANT: Boyd, Andrew W.
; APPLICANT: Simpson, Richard J.
; APPLICANT: Wicks, Ian
; APPLICANT: Ward, Larry D.
; APPLICANT: Wilkinson, David
; TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715, 106
; FILING DATE: 18-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167, 919
; FILING DATE: 18-APR-1994
; APPLICATION NUMBER: PK6841 (AU)
; FILING DATE: 21-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PK9992 (AU)
; FILING DATE: 12-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00294
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-715-106-11

Query Match 71.1%; Score 27; DB 3; Length 432;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 SRDTEVL 8
111111
DB 177 SRDDEVL 183

RESULT 13
US-09-150-440-1
Sequence 1, Application US/09150440
Patent No. 6204041
GENERAL INFORMATION:
APPLICANT: Zalkin, Howard
APPLICANT: Smith, Janet L.
APPLICANT: Switzer, Robert L.
TITLE OF INVENTION: DEREGULATION OF GLUTAMINE PRPP AMIDOTRANSFERASE
FILE REFERENCE: 3220-60979
CURRENT APPLICATION NUMBER: US/09/150,440
CURRENT FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentlin Ver. 2.0
SEQ ID NO 1
LENGTH: 465
TYPE: PRP
ORGANISM: Bacillus subtilis
PUBLICATION INFORMATION:
AUTHORS: Makaroff, Christopher A.
AUTHORS: Zalkin, Howard
AUTHORS: Switzer, Robert L.
AUTHORS: Vollmer, Steven J.
TITLE: Cloning of the Bacillus Subtilis Glutamine
TITLE: Phosphoribosylhydrophosphate Amidotransferase Gene in
TITLE: Escherichia Coli
JOURNAL: J. Biol. Chem.
VOLUME: 258
ISSUE: 17
PAGES: 10586-10593
DATE: 1983-09-10
US-09-150-440-1

Query Match 71.1%; Score 27; DB 4; Length 465;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 SRDTEVL 8
111111
DB 125 SSDTEVL 131

RESULT 14
US-08-914-999-12
Sequence 12, Application US/08914999
Patent No. 6346406
GENERAL INFORMATION:
APPLICANT: Ryazanov, Alexey G.
APPLICANT: Halt, William N.
APPLICANT: Pavur, Karen S.

TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
TITLE OF INVENTION: AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,999
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: C. elegans
US-08-914-999-12

Query Match 71.1%; Score 27; DB 4; Length 760;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSRDTE 6
111111
DB 476 QTRDTE 481

RESULT 15
US-08-914-999-10
Sequence 10, Application US/08914999
Patent No. 6346406
GENERAL INFORMATION:
APPLICANT: Ryazanov, Alexey G.
APPLICANT: Halt, William N.
APPLICANT: Pavur, Karen S.
TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
TITLE OF INVENTION: AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.30

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,999
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 601-1-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: C. elegans
; US-08-914-999-10

Query Match 71.1%; Score 27; DB 4; Length 768;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSRDTE 6
1:||||
Db 476 QTRDTE 481

Search completed: August 31, 2002, 12:15:45
Job time: 141 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 31, 2002, 12:15:30 ; Search time 25.05 Seconds
(without alignments)
55.248 Million cell updates/sec

Title: US-09-516-728-1
Perfect score: 38
Sequence: 1 QSRDREVL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mmc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvirus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	425	4 Q9NPR5	Q9NPR5 homo sapien
2	38	100.0	1337	4 Q15255	Q15255 homo sapien
3	33	86.8	634	11 Q9D0H7	Q9D0H7 mus musculu
4	32	84.2	428	3 Q60140	Q60140 schizosacch
5	31	81.6	252	10 Q9S226	Q9S226 arabidopsis
6	31	81.6	335	16 Q970A6	Q970A6 streptococc
7	31	81.6	446	8 Q9BAK0	Q9BAK0 lepidothamn
8	31	81.6	448	8 Q32326	Q32326 tradescanti
9	31	81.6	436	8 Q9SCG3	Q9SCG3 tradescanti
10	31	81.6	539	4 Q9HCR8	Q9HCR8 homo sapien
11	31	81.6	543	5 Q9W2R1	Q9W2R1 drosophila
12	30	81.6	689	4 Q9HB58	Q9HB58 homo sapien
13	30	78.9	105	13 Q91404	Q91404 xenopus lae
14	30	78.9	198	2 Q46025	Q46025 corrynebacte
15	30	78.9	218	15 Q90M04	Q90M04 human immun
16	30	78.9	251	5 Q9U247	Q9U247 caenorhabdi

17	30	78.9	425	5 Q9XU14	Q9XU14 caenorhabdi
18	30	78.9	448	8 Q9BAI3	Q9BAI3 prunomylis
19	30	78.9	503	11 Q9CY96	Q9CY96 mus musculu
20	30	78.9	513	4 Q9BU59	Q9BU59 homo sapien
21	30	78.9	513	4 Q9NVD1	Q9NVD1 homo sapien
22	30	78.9	513	11 Q9D118	Q9D118 mus musculu
23	30	78.9	513	11 Q9J470	Q9J470 mus musculu
24	30	78.9	513	11 Q99M63	Q99M63 rattus norv
25	30	78.9	519	13 Q91911	Q91911 brachydanio
26	30	78.9	576	10 Q9C923	Q9C923 arabidopsis
27	30	78.9	1012	5 Q97035	Q97035 hydra magni
28	30	78.9	1170	13 Q57612	Q57612 tetraodon f
29	30	78.9	1403	11 Q9QXG1	Q9QXG1 mus musculu
30	30	78.9	1911	5 Q9W4M7	Q9W4M7 drosophila
31	30	78.9	2712	10 Q9S874	Q9S874 arabidopsis
32	29	76.3	63	2 P72450	P72450 streptococc
33	29	76.3	77	3 Q96WB9	Q96WB9 fusarium sp
34	29	76.3	152	2 Q9KY21	Q9KY21 streptomyc
35	29	76.3	336	10 Q9SU91	Q9SU91 arabidopsis
36	29	76.3	361	5 Q9W1P2	Q9W1P2 drosophila
37	29	76.3	399	10 Q9SEZ3	Q9SEZ3 arabidopsis
38	29	76.3	403	5 Q9GCP3	Q9GCP3 echinococcu
39	29	76.3	446	8 Q9BAIL	Q9BAIL retrophyllu
40	29	76.3	524	2 Q93GK2	Q93GK2 klebsiella
41	29	76.3	538	4 Q15079	Q15079 homo sapien
42	29	76.3	765	12 Q9JG58	Q9JG58 tt virus . p
43	29	76.3	765	12 Q9JG55	Q9JG55 tt virus . p
44	29	76.3	765	12 Q9JG52	Q9JG52 tt virus . p
45	29	76.3	909	3 Q9P4U1	Q9P4U1 agarius bi

ALIGNMENTS

RESULT 1

Q9NPR5 PRELIMINARY; PRT; 425 AA.
ID Q9NPR5
AC Q9NPR5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PTPKJ, PROTEIN TYROSINE PHOSPHATASE RECEPTOR J, ETA (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Andreu N., Estivill X., Escarceller M., Sunoy L.;
RN Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Aufray C., Ansoerge W., Ballabio A., Estivill X., Gibson K.,
RA Lehnach H., Poustka A., Lundeberg J.;
RT "The European IMAGE consortium for integrated Molecular analysis of
RT human gene transcripts.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL359057; CAB94390.1;
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 2.
KW Receptor.
FT NON_TER
FT SEQUENCE 425 AA; 45078 MW; BD1ACA5D345B7027 CRC64;

Query Match 100.0%; Score 38; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSRDREVL 8
|||||||
Db 324 QSRDREVL 331

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RESULT 2
ID 015255 PRELIMINARY: PRT: 1337 AA.
AC 015255;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=95086212; PubMed=7994032;
RA Honda H.;
RT "Molecular cloning, characterization, and chromosomal localization of
RT a novel protein-tyrosine phosphatase, Hppeta."
RL EMBL: D37781; BAA07035.1; -.
DR HSSP: P18052; IYFO.
DR InterPro: IPR001395; Aldo_ket_red.
DR InterPro: IPR003961; FN_LIT.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_prot_phphatase.
DR Pfam: PF00041; fn3; 5.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PRTPHPTASE.
DR SMART: SM0060; FN3; 6.
DR SMART; SM00194; PTPc; 1.
DR PROSITE: PS00063; ALDOKEO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
DR HydroLase; Signal; trans peptide.
KM SIGNAL
FT SIGNAL 19
FT TRANSIT 971 995 POTENTIAL.
SQ SEQUENCE 1337 AA; 145802 MW; BA7EA3EE32961CEA CRC64;

Query Match 100.0%; Score 38; DB 4; Length 1337;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSRDFEVL 8
DB 324 QSRDFEVL 331

RESULT 3
ID 09D0H7 PRELIMINARY: PRT: 654 AA.
AC 09D0H7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 2610016F07RIK PROTEIN.
GN POVI OR 2610016F07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21083660; PubMed=11217851;
RA Arakawa T.; Shigaawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.;
RA Arakawa T.; Hara A.; Fukunishi Y.; Kono H.; Adachi J.; Fukunaka S.;
RA Aizawa K.; Izawa M.; Nishi K.; Kiyosawa H.; Kondo S.; Yamanaka I.;
RA Saito T.; Okazaki Y.; Gojobori T.; Bono H.; Kasukawa T.; Saito R.;
RA Kadota K.; Matsuda H.A.; Ashburner M.; Batalov S.; Casavant T.;

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RA Fleischmann W.; Gaasterland T.; Gissi C.; King B.; Kochia H.;
RA Kuehl P.; Lewis S.; Matsuo Y.; Nikaio I.; Pesole G.; Quackenbush J.;
RA Schriml L.M.; Staubli F.; Suzuki R.; Tomita M.; Wagner L.; Washio T.;
RA Sakai K.; Okido T.; Furuno M.; Aono H.; Baldarelli R.; Barsh G.;
RA Blake J.; Boffelli D.; Bojunga N.; Carninci P.; de Bernaldo M.F.;
RA Brownstein M.J.; Bult C.; Fletcher C.; Fujita M.; Gariboldi M.;
RA Gustincich S.; Hill D.; Hofmann M.; Hume D.A.; Kamuya M.; Lee N.H.;
RA Lyons P.; Marchionni L.; Mashima J.; Mazzarelli J.; Mombaerts P.;
RA Nordone P.; Ring B.; Ringwald M.; Rodriguez I.; Sakamoto N.;
RA Sasaki H.; Sato K.; Schoenbach C.; Seya T.; Shibata Y.; Storch K.-F.;
RA Suzuki H.; Toyono-Oka K.; Wang K.H.; Weltz C.; Whitaker C.; Wilming L.;
RA Wynshaw-Boris A.; Yoshida K.; Hasegawa Y.; Kawaji H.; Kohsaki S.;
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK011417; BAB27605.1; -.
DR MGD: MGI:1931352; Povl.
SQ SEQUENCE 654 AA; 72589 MW; FFD7521C2B2518BB CRC64;

Query Match 86.8%; Score 33; DB 11; Length 654;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SRDTEVL 8
DB 215 SRDTEVL 221

RESULT 4
ID 060140 PRELIMINARY: PRT: 428 AA.
AC 060140;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 49.1 KDA PROTEIN.
GN SPBC18H10.09.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN=972H-;
RA Lyne M.; Rajandream M.A.; Barrell B.G.; Badcock K.; Churcher C.M.;
RL Submitted (MAR-1998) to the EMBL/genbank/DBJ databases.
DR EMBL: AL022304; CAA18406.1; -.
KM Hypothetical protein.
SQ SEQUENCE 428 AA; 49074 MW; DE9FD835A4A83418 CRC64;

Query Match 84.2%; Score 32; DB 3; Length 428;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSRDFEVL 8
DB 150 QSRDFEVL 157

RESULT 5
ID 09SZ26 PRELIMINARY: PRT: 252 AA.
AC 09SZ26;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 27.8 KDA PROTEIN.
GN I73G19.60 OR AT4G25680.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```


OC Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Schueller C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Pohl T., Weizenegger T., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050400; CAB43699.1; -
 DR EMBL; AL161563; CAB81378.1; -
 KW Hypothetical protein
 SO SEQUENCE 252 AA; 27803 MW; 3AC14BE12DF4D0C5 CRC64;

Query Match 81.6%; Score 31; DB 10; Length 252;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSRDTEVL 8
 Db 242 QSRSDVL 249
 RESULT 6
 ID 0970A6 PRELIMINARY; PRT; 335 AA.
 AC 0970A6;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE V-TYPE SODIUM ATP SYNTHASE, SUBUNIT C.
 GN SPI319.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelein H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Hatt D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolony J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radeanu D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae";
 RL Science 293:498-506(2001).
 DR EMBL; AE007430; AAK75417.1; -
 DR TIGR; SPI319; -
 KW Complete proteome.
 SO SEQUENCE 335 AA; 38682 MW; 5825DBF919EFD405 CRC64;

Query Match 81.6%; Score 31; DB 16; Length 335;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSRDTEVL 8
 Db 31 QSKDTEVL 38

RESULT 7
 ID 09BAK0 PRELIMINARY; PRT; 446 AA.
 AC 09BAK0;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE RIBULOSE BIPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
 DE LARGE SUBUNIT) (FRAGMENT).
 GN RBCL.
 OS Lepidochamnus fonkii.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Podocarpaceae;
 OC Lepidochamnus.
 OX NCBI_TaxID=120595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Conran J.G., Wood G.A., Martin P.G., Dowd J.M., Quinn C.J.,
 RA Gadek P.A., Price R.A.;
 RT "Generic relationships within and between the gymnosperm families
 RT Podocarpaceae and Phyllocladaceae based on an analysis of the
 RT chloroplast gene rbcl.";
 RL Aust. Syst. Bot. 0:0-0(2000).
 CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-
 CC RIBULOSE 1,5-BIPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
 CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 CC ACTIVE SITE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BIPHOSPHATE + CO(2) = 2 3-
 CC PHOSPHO-D-GLYCERATE.
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BIPHOSPHATE + O(2) = 3-
 CC PHOSPHO-D-GLYCERATE + 2-PHOSPHOGYCOLATE.
 CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
 DR EMBL; AF249642; AAK9524.1; -
 DR HSSP; P04718; IRUS.
 DR InterPro: IPR000685; Rubisco_large.
 DR Pfam; PF00016; Rubisco_large.1.
 DR Pfam; PF02788; Rubisco_large.NF.1.
 DR ProSite; PS00157; Rubisco_large.1.
 KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
 KW Oxidoreductase; Photorespiration; Photosynthesis.
 FT NON_TER 1 1
 FT 446 446
 SO SEQUENCE 446 AA; 49394 MW; 1FB6045EB477F236 CRC64;

Query Match 81.6%; Score 31; DB 8; Length 446;
 Best Local Similarity 62.5%; Pred. No. 62;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSRDTEVL 8
 Db 20 QSKDTEVL 27
 RESULT 8
 ID 033236 PRELIMINARY; PRT; 448 AA.
 AC 033236;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE RIBULOSE BIPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
 DE LARGE SUBUNIT) (FRAGMENT).
 GN RBCL.

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Honck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster.",
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003452; AAF46629.1; -.
 DR HSSP: P08659; 1LC1.
 DR FLYBase: FBgn003453; CG9993.
 DR InterPro: IPR000873; AMP-bind.
 DR InterPro: IPR000508; Peptidase_S26.
 DR Pfam: PF00501; AMP-binding; 1.
 DR PROSITE: PS00761; SPASE_1_3; 1.
 SQ SEQUENCE 543 AA; 60344 MW; A6A9B0E1457DC9F CRC64;

Query Match 81.6%; Score 31; DB 5; Length 543;
 Best Local Similarity 85.7%; Pred. No. 77;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 QSRDREV 7
 Db 429 QSRDREV 435
 RESULT 12
 Q9HB58 PRELIMINARY; PRT; 689 AA.
 AC Q9HB58.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TRANSCRIPTIONAL COACTIVATOR SP110.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bloch D.B., Nakajima A., Gulick T., Chiche J., Orth D.,
 RA de la Monte S.M., Bloch K.D.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF280095; AAG09826.1; -.
 DR InterPro: IPR001487; Bromodomain.
 DR InterPro: IPR001965; PHD.
 DR InterPro: IPR000770; SAND.
 DR Pfam: PF00628; PHD; 1.
 DR SMART: SM00297; BROMO; 1.
 DR SMART: SM00249; PHD; 1.
 DR SMART: SM00258; SAND; 1.

SQ SEQUENCE 689 AA; 78474 MW; 8F64CEDC1F0DD1FB CRC64;
 Query Match 81.6%; Score 31; DB 4; Length 689;
 Best Local Similarity 75.0%; Pred. No. 99;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QSRDREV 8
 Db 113 QSRDREV 120
 RESULT 13
 Q91404 PRELIMINARY; PRT; 105 AA.
 AC Q91404.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE XK ENDO B HOMOLOG PROTEIN (FRAGMENT).
 GN XK ENDO B HOMOLOG.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-95290493; PubMed-7772598;
 RA Adelti N., Ito T., Koga C., Kito K., Sakaki Y., Shiohawa K.,
 RA "Differential display analysis of gene expression in developing
 RT embryos of Xenopus laevis.",
 RL Blochim. Biophys. Acta 1262:43-51(1995).
 CC -1- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
 DR EMBL: S78089; AAB34522.1; -.
 DR InterPro: IPR001664; IF.
 DR Pfam: PF00038; Filament; 1.
 DR PROSITE: PS00226; IF; 1.
 KW Coiled coil; Intermediate filament.
 FT NON_TER 1
 SQ SEQUENCE 105 AA; 11896 MW; CDD924315223514A CRC64;

Query Match 78.9%; Score 30; DB 13; Length 105;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QSRDREV 8
 Db 96 ESRDREV 103
 RESULT 14
 Q46025 PRELIMINARY; PRT; 198 AA.
 AC Q46025.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE IRON REPRESSIBLE POLYPEPTIDE.
 GN DIRA.
 OS Corynebacterium diptheriae.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
 CC Corynebacterium.
 OX NCBI_TaxID=1717;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C7.
 RA MEDLINE-95286547; PubMed-7768861;
 RA Tai S.-S., Zhu Y.Y.,
 RT "Cloning of a Corynebacterium diptheriae iron-repressible gene that
 shares sequence homology with the AnpC subunit of alkyl hydroperoxide

RT reductase of *Salmonella typhimurium*.;
RL J. Bacteriol. 177:3512-3517(1995).
DR EMBL; U18620; AAA86946.1; -
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 198 AA; 22312 MW; 7A09DCB4A07705DD CRC64;

Query Match 78.9%; Score 30; DB 2; Length 198;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSRDTEVL 8
DB 76 QDRDTQIL 83

RESULT 15

ID Q90M04 PRELIMINARY; PRT; 218 AA.
AC Q90M04;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human Immunodeficiency Virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM1014;
RA Herring B.L., Dwyer D.E.;
RT "Australian HIV-1 env subtypes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF400083; AAK91742.1; -
FT NON_TER 1 1
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 24303 MW; E8F49BA240566450 CRC64;

Query Match 78.9%; Score 30; DB 15; Length 218;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSRDTEV 7
DB 198 ESRDTEI 204

Search completed: August 31, 2002, 12:19:09
Job time: 219 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 31, 2002, 12:15:50 ; Search time 10.32 Seconds
(without alignments)
30.015 Million cell updates/sec

Title: US-09-516-728-1

Perfect score: 38
Sequence: 1 OSRDREV.L 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	1337	1 PPTJ_HUMAN	Q12913 homo sapien
2	31	81.6	1649	1 YG44_SCHPO	O60179 schizosacch
3	30	78.9	203	1 YC11_AOUAE	O67264 aquiflex aeo
4	29	76.3	430	1 AROA_MYCLE	O96c13 mycobacteri
5	29	76.3	450	1 AROA_MYCTU	P22487 mycobacteri
6	29	76.3	499	1 CPDE_CANPA	O28473 canis famli
7	29	76.3	500	1 CPDG_CANPA	O64403 canis porce
8	29	76.3	851	1 MOUTS_STRPY	O99x18 streptococc
9	29	76.3	1636	1 YN37_YEAST	P48563 saccharomyc
10	29	76.3	3924	1 ANK2_HUMAN	O01484 homo sapien
11	28	73.7	75	1 VC12_SPVKA	P33221 swinepox vi
12	28	73.7	242	1 PDXJ_SYNG3	P72776 synechocyst
13	28	73.7	334	1 Y456_MYCGE	P47694 mycoplasma
14	28	73.7	362	1 HA19_CANPA	P18466 canis famli
15	28	73.7	394	1 RBL_ALIPL	P34767 alyisma plan
16	28	73.7	414	1 RBL_ONYJA	O36610 onychium ja
17	28	73.7	416	1 RBL_ARTBA	P43225 arthropiari
18	28	73.7	417	1 RBL_ACRAT	P43225 arthropiari
19	28	73.7	420	1 RBL_ANEME	O31674 anemia mexi
20	28	73.7	441	1 RBL_BEGMS	P28258 begonia met
21	28	73.7	443	1 RBL_ABIFI	O78258 abies firma
22	28	73.7	443	1 RBL_ABIHO	O78259 abies homol
23	28	73.7	443	1 RBL_ABIHR	O78261 abies marie
24	28	73.7	443	1 RBL_ABITA	O78262 abies sachc
25	28	73.7	443	1 RBL_ABIYE	O78260 abies veitc
26	28	73.7	444	1 CEB_DROME	O02637 drosophila
27	28	73.7	444	1 RBL_GINBI	P48704 ginkgo billo
28	28	73.7	444	1 RBL_WELMI	P48719 welwitschia
29	28	73.7	449	1 NDOB_PSEPU	P23094 pseudomonas
30	28	73.7	451	1 CEB_DROVI	O02638 drosophila
31	28	73.7	453	1 RBL_HYDFO	O33397 hydnophytum
32	28	73.7	455	1 RBL_LUPAE	P92396 lupinus alb
33	28	73.7	455	1 RBL_LUPDE	P92401 lupinus den

34	28	73.7	455	1 RBL_LUPMI	P92406 lupinus mic
35	28	73.7	460	1 RBL_CRYIA	P48696 cryptomeria
36	28	73.7	460	1 RBL_CUNIA	O32026 cunilughami
37	28	73.7	465	1 RBL_EPHTW	O32223 epinedra lwe
38	28	73.7	465	1 RBL_QUITN	P28446 quiscualls
39	28	73.7	466	1 RBL_HEDHE	P28421 hedera heli
40	28	73.7	467	1 RBL_CEDAT	O9696 cedrus atla
41	28	73.7	468	1 RBL_ANTVS	O31859 anthocercis
42	28	73.7	468	1 RBL_CAPBA	O31951 capsicum ba
43	28	73.7	468	1 RBL_CATSP	O33383 catesbaea s
44	28	73.7	468	1 RBL_DATST	P48698 datura stra
45	28	73.7	468	1 RBL_NOLSP	O32699 nolana spat

ALIGNMENTS

```

RESULT 1
PPTJ_HUMAN
ID PPTJ_HUMAN STANDARD: PRT; 1337 AA.
AC Q12913; Q15255;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
DE (HPTP eta) (Density enhanced phosphatase-1) (DEP-1) (CD148 antigen).
GN PPTJ OR DEP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=95024024; PubMed=7937872;
RA Oestman A., Yang Q., Tonks N.K.;
RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
RT is enhanced with increasing cell density.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
RN [2]
RP MEDLINE=95086212; PubMed=7994032;
RA Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
RT "Molecular cloning, characterization, and chromosomal localization of
RT a novel protein-tyrosine phosphatase, HPTP eta.";
RL Blood 84:4186-4194(1994).
CC -! FUNCTION: MAY CONTRIBUTE TO THE MECHANISM OF CONTRACT INHIBITION OF
CC CELL GROWTH.
CC -! CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! PTM: N- AND O-GLYCOSYLATED.
CC -! SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
CC -! SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -! DATABASE: NAME=PROW; NOTE=CD guide CD148 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".
CC -----
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CC -----
DR EMBL: U10886; AA36687.1; -.
DR EMBL: D37781; BA07035.1; -.
DR HSSP: P18052; IYFO.
DR MIM: 600925; -.
DR InterPro: IPR003961; FY_III.
DR InterPro: IPR000387; Tyr_phosphatase.
DR InterPro: IPR000242; Tyr_prot_phptase.
DR Pfam: PF00041; In3; 5.
DR Pfam: PF00102; Y_phosphatase; 1.

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DR PRINTS: PRO0700; PRTYPHPTASE.
DR SMART: SM00060; FN3; 6.
DR PROSITE: PS00194; PTPC; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Signal; Glycoprotein; Transmembrane; Repeat; Hydrolyase.
FT SIGNAL 1 35
FT CHAIN 36 1337
FT DOMAIN 36 975
FT TRANSMEM 976 996
FT DOMAIN 997 1337
FT DOMAIN 119 199
FT DOMAIN 366 446
FT DOMAIN 454 532
FT DOMAIN 540 615
FT DOMAIN 626 710
FT DOMAIN 1065 1337
FT ACT_SITE 1239 1239
FT CARBOHYD 72 72
FT CARBOHYD 82 82
FT CARBOHYD 93 93
FT CARBOHYD 104 104
FT CARBOHYD 142 142
FT CARBOHYD 172 172
FT CARBOHYD 192 192
FT CARBOHYD 231 231
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FT CARBOHYD 431 431
FT CARBOHYD 501 501
FT CARBOHYD 525 525
FT CARBOHYD 536 536
FT CARBOHYD 582 582
FT CARBOHYD 603 603
FT CARBOHYD 618 618
FT CARBOHYD 628 628
FT CARBOHYD 637 637
FT CARBOHYD 666 666
FT CARBOHYD 669 669
FT CARBOHYD 761 761
FT CARBOHYD 772 772
FT CARBOHYD 784 784
FT CARBOHYD 790 790
FT CARBOHYD 824 824
FT CARBOHYD 910 910
FT CARBOHYD 937 937
FT CONFLICT 261 261
FT CONFLICT 918 918
FT CONFLICT 929 929
FT SEQUENCE 1337 AA; 145985 MW; E686DE6D1F64236E CRC64;

Query Match
Best Local Similarity 100.0%; Score 38; DB 1; Length 1337;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSRDTEVL 8
DB 324 QSRDTEVL 331

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DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hypothetical 186.4 kDa protein C23E6.04c in chromosome II.
GN SPBC23E6.04C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Pohl T.;
RL Submitted (May-1998) to the EMBL/Genbank/DBD databases.
CC -1- SIMILARITY: BELONGS TO THE BAP28 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 HEAT REPEAT.
CC -----
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CC -----
DR EMBL: AL023287; CA18872.1; -.
DR InterPro: IPR000357; HEAT_repeat.
DR PROSITE: PS00077; HEAT_REPEAT; 1.
KW Hypothetical protein.
FT REPEAT 1608 1646
FT SEQUENCE 1649 AA; 186409 MW; 6B4ED373125216D9 CRC64;

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Query Match
Best Local Similarity 81.6%; Score 31; DB 1; Length 1649;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSRDTEV 7
DB 524 QSRDTEV 530

RESULT 3
ID YC11_AQUAE STANDARD; PRT; 203 AA.
AC 067264;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hypothetical protein AQ_1211.
GN AQ_1211.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anuj M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- SIMILARITY: TO A.AEOLICUS AQ_820 AND AQ_1583.
CC -----
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DR EMBL: AE000729; AAC07233.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 203 AA; 23960 MW; BFCCE047E973AF29 CRC64;

Query Match 78.9%; Score 30; DB 1; Length 203;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QSRDREVL 8
 Db 71 QKRDSVL 78

RESULT 4
 AROA_MYCLE STANDARD; PRT; 430 AA.
 ID AROA_MYCLE
 AC 09CCT3;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
 enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
 GN AROA OR M0792.
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holtroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RT Nature 409:1007-1011(2001).
 RL Nature 409:1007-1011(2001).
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
 CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -1- SUBUNIT: MONOMER (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: AL583919; CAC30301.1; -
 DR Leproma; M0792; -
 DR InterPro: IPR001986; EPSP_synthase.
 DR Pfam: PF00275; EPSP_synthase; 1.
 DR ProDom: PD001867; EPSP_synthase; 1.
 DR PROSITE: PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE: PS00885; EPSP_SYNTHASE_2; 1.
 KW Aromatic amino acid biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 430 AA; 44557 MW; 445975BA53DC74D9 CRC64;

Query Match 76.3%; Score 29; DB 1; Length 430;
 Best Local Similarity 62.5%; Pred. No. 43;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSRDREVL 8
 Db 53 RSRDREVL 60

RESULT 5
 AROA_MYCTU STANDARD; PRT; 450 AA.
 ID AROA_MYCTU
 AC P22487;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
 enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
 GN AROA OR RV3227 OR M3324 OR MTCY20B11.02.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=91072223; PubMed=2123856;
 RA Garde T., Jones C., Charles I.G., Dougan G., Young D.;
 RT "Cloning and characterization of the *aroA* gene from *Mycobacterium*
 RT tuberculosis";
 RL J. Bacteriol. 172:6774-6782(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Baddock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., Maclean J., Moule S., Murphy L.,
 RA Oliver S., Osborne K., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton J., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 RT complete genome sequence.";
 RT Nature 393:537-544(1998).
 RL Nature 393:537-544(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 RT laboratory strains.";
 RT Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
 CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: X52269; CAA36510.1; -
 DR EMBL: M62708; AAA25356.1; -
 DR EMBL: Z95121; CAB08328.1; -

DR EMBL: A5007144; AAK47667.1; -.
 DR PIR: A37807; A37807.
 DR TIGR: M33324; -.
 DR TubercuList; RV3227; -.
 DR InterPro: IPR001986; EPSP_synthase.
 DR Pfam: PF00275; EPSP_synthase.1.
 DR PRODOM: PD001867; EPSP_synthase.1.
 DR PROSITE: PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE: PS00885; EPSP_SYNTHASE_2; 1.
 KW Aromatic amino acid biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 450 AA; 46425 MW; 27BB86F9412A07D5 CRC64;

Query Match 76.3%; Score 29; DB 1; Length 450;
 Best Local Similarity 62.5%; Pred. No. 45;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSRDTEVL 8
 DB 51 RSRDTELM 58

RESULT 6
 CPDF_CANFA STANDARD; PRT; 499 AA.
 AC 029473; 002859;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cytochrome P450 2D15 (EC 1.14.14.1) (CYPI1D15) (P450 DUT2).
 GN CYP2D15.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=LIVER;
 RX MEDLINE=95305574; PubMed=7786018;
 RA Sakamoto K., Kirita S., Baba T., Nakamura Y., Yamazoe Y., Kato R.,
 RA Takahata A., Matsubara T.;
 RT "A new cytochrome P450 form belonging to the CYP2D in dog liver
 RT microsomes: purification, cDNA cloning, and enzyme
 RT characterization.";
 RL Arch. Biochem. Biophys. 319:372-382(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BEAGLE;
 RX MEDLINE=98162950; PubMed=9504424;
 RA Tasaki T., Nakamura A., Itoh S., Ohashi K., Yamamoto Y., Masuda M.,
 RA Iwata H., Kazusaka A., Kametaki T., Fujita S.;
 RT "Expression and characterization of dog CYP2D15 using baculovirus
 RT expression system.";
 RL J. Biochem. 123:162-168(1998).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=98389575; PubMed=9721180;
 RA Rousset F., Dulgann D.B., Lawton M.P., Obach R.S., Strick C.A.,
 RA Tweedie D.J.;
 RT "Expression and characterization of canine cytochrome P450 2D15.";
 RL Arch. Biochem. Biophys. 357:27-36(1998).
 CC -1- FUNCTION: HIGH ACTIVITY FOR THE HYDROXYLATION OF BUNITROL AND
 CC IMPRAIRINE: LOW ACTIVITY ON DEBRISOQUINE.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: LIVER. ALSO DETECTED IN SEVERAL OTHER TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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 CC -----

DR EMBL: D17397; BAA04220.1; -.
 DR EMBL: AB004268; BAA20357.1; -.
 DR HSSP: P00179; 1D16.
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT INIT_MET 0
 FT BINDING 445 445 HEME (BY SIMILARITY).
 SQ SEQUENCE 499 AA; 56301 MW; 27E352B5B309E7F1 CRC64;

Query Match 76.3%; Score 29; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRDTEV 7
 DB 381 SRDTEV 386

RESULT 7
 CPDG_CANFO STANDARD; PRT; 500 AA.
 AC 064403; 054866;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cytochrome P450 2D16 (EC 1.14.14.1) (CYPI1D16).
 GN CYP2D16.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognath; Cavidae; Cavia.
 OX NCBI_Taxid=10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-38.
 RC STRAIN=13; TISSUE=Adrenal cortex;
 RX MEDLINE=95251703; PubMed=7733969;
 RA Jiang Q., Voigt J.M., Colby H.D.;
 RT "Molecular cloning and sequencing of a guinea pig cytochrome P450 2D
 RT (CYP2D16) in guinea pig adrenal gland.";
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HARTLEY WHITE; TISSUE=Adrenal gland;
 RA Sun Y., Voigt J.M., Pierce J.C., Colby H.D.;
 RT "The gene sequence of a xenobiotic metabolism-related cytochrome P450
 RT isozyme (CYP2D16) in guinea pig adrenal gland.";
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
 CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
 CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
 CC ACIDS, AND XENOBIOTICS.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE INNER ZONE OF
 CC THE ADRENAL CORTEX.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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CC -----
DR EMBL: U21486; AAA68479.1; -.
DR EMBL: AF020345; AAB94568.1; -.
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT DOMAIN 81 84 POLY-VAL.
FT BINDING 446 446 HEME (BY SIMILARITY).
FT CONFLICT 123 123 I -> V (IN REF. 2).
FT CONFLICT 127 127 Y -> N (IN REF. 2).
FT CONFLICT 148 148 G -> R (IN REF. 2).
SQ SEQUENCE 500 AA; 55800 MW; 2429247EA9BF6B24 CRC64;

Query Match
Best Local Similarity 76.3%; Score 29; DB 1; Length 500;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRDTEY 7
DB 382 SRDTEY 387

RESULT 8
MUTS_STRPY
ID MUTS_STRPY STANDARD; PRT; 851 AA.
AC 099XL8;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE DNA mismatch repair protein MUTS.
GN MUTS OR SP22148.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;
RC MEDLINE=21192684; PubMed=11296296;
RA Ferretti J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najaf F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- FUNCTION: This protein is involved in the repair of mismatches in
CC DNA. It is possible that it carries out the mismatch recognition
CC step. This protein has a weak ATPase activity (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
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CC -----
DR EMBL: AE006633; AAK34785.1; -.
DR InterPro: IPR00432; MUTS_C.
DR InterPro: IPR002863; MUTS_N.
DR Pfam: PF00488; MUTS_C; 1.
DR Pfam: PF01624; MUTS_N; 1.
DR ProDom: PD001263; MUTS_C; 1.
DR SMART: SM00534; MUTS_C; 1.
DR SMART: SM00533; MUTS_C; 1.
DR PROSITE: PS00486; DNA_MISMATCH_REPAIR_2; 1.
KW DNA repair; ATP-binding; DNA-binding; Complete proteome.

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FT NP_BIND 602 609 ATP (POTENTIAL).
SQ SEQUENCE 851 AA; 95470 MW; 737D51CBDDFEAF0A CRC64;

Query Match
Best Local Similarity 76.3%; Score 29; DB 1; Length 851;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OSRDTEYL 8
DB 787 OSRDTEYL 794

RESULT 9
MUTS_YEAST
ID MUTS_YEAST STANDARD; PRT; 1636 AA.
AC P48563;
DT 01-FEB-1996 (Rel. 33; Created)
DT 01-FEB-1996 (Rel. 33; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE Hypothetical 186.8 kDa protein in CLA4-FUS4 intergenic region.
GN YNL297C OR N0453.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / FY1679;
RC MEDLINE=96132033; PubMed=8553702;
RA Maurer K.C.T., Urbanus J.H.M., Planta R.J.;
RT "Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
RT carrying a ribosomal protein gene cluster, the genes encoding a
RT plasma membrane protein and a subunit of replication factor C, and a
RT novel putative serine/threonine protein kinase gene.";
RL Yeast 11:1303-1310(1995).
CC -!- SIMILARITY: SOME, TO S.POMBE SPAC23D3.13C.
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CC -----
DR EMBL: U23084; AAC49101.1; -.
DR EMBL: Z71573; CAA96214.1; -.
DR SGD: S0005241; YNL297C.
KW Hypothetical protein.
SQ SEQUENCE 1636 AA; 186834 MW; F0B3D8E6BD094D6 CRC64;

Query Match
Best Local Similarity 76.3%; Score 29; DB 1; Length 1636;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRDTEYL 8
DB 1267 SRDTEYL 1273

RESULT 10
ANK2_HUMAN
ID ANK2_HUMAN STANDARD; PRT; 3924 AA.
AC Q01484; Q01485;
DT 01-APR-1993 (Rel. 25; Created)
DT 01-APR-1996 (Rel. 34; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RX MEDLINE=91302466; PubMed=1830053;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.,
RT "Isolation and characterization of cDNAs encoding human brain
RL ankyrin reveal a family of alternatively spliced genes.";
RN J. Cell Biol. 114:241-253(1991).
RP REVISIONS.
RA Carpenter S.;
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844;
RA Chan W., Kordeli E., Bennett V.;
RT "440-kD ankyrinB: structure of the major developmentally regulated
RL domain and selective localization in unmyelinated axons.";
RN J. Cell Biol. 123:1463-1473(1993).
RN (4)
RP SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE=92009921; PubMed=1833308;
RA Tse W.T., Wenninger J.C., Tang-Feng T.L., Francke U., Sahr K.E.,
RT Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
RL ankyrin gene.";
RT Genomics 10:858-866(1991).
CC -I- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements. Also bind to cytoskeletal proteins.
CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -I- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN.
CC -I- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -I- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL; X56957; CAA40278.1; -;
DR EMBL; X56958; CAA40279.2; -;
DR EMBL; Z26634; CAA42644.1; -;
DR EMBL; M37123; AAA62828.1; -;
DR PIR; S14533; S14533;
DR PIR; A39643; A39643;
DR PIR; B39643; B39643;
DR PIR; S14569; S14569;
DR HSP; C00421; IAWC.
DR MIM; 106410; -;
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZUS.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PR00791; ZUS; 1.
DR PRINTS; PR01415; ANKTRIN.
DR SMART; SM00248; ANK; 21.
DR SMART; SM00218; ZUS; 1.
DR PROSITE; PSS0088; ANK_REPEAT; 20.
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.

KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW Phosphorylation.
FT REPEAT 63 92 ANK 1.
FT REPEAT 96 125 ANK 2.
FT REPEAT 129 158 ANK 3.
FT REPEAT 162 191 ANK 4.
FT REPEAT 193 220 ANK 5.
FT REPEAT 232 261 ANK 6.
FT REPEAT 265 294 ANK 7.
FT REPEAT 298 327 ANK 8.
FT REPEAT 331 360 ANK 9.
FT REPEAT 364 393 ANK 10.
FT REPEAT 397 426 ANK 11.
FT REPEAT 430 459 ANK 12.
FT REPEAT 463 492 ANK 13.
FT REPEAT 496 525 ANK 14.
FT REPEAT 529 558 ANK 15.
FT REPEAT 562 591 ANK 16.
FT REPEAT 595 624 ANK 17.
FT REPEAT 628 657 ANK 18.
FT REPEAT 661 690 ANK 19.
FT REPEAT 723 756 ANK 20.
FT REPEAT 760 789 ANK 21.
FT REPEAT 793 822 ANK 22.
FT REPEAT 850 879 ANK 23.
FT DOMAIN 1773 1950 REPEAT-RICH REGION.
FT REPEAT 1773 1784 REPEAT A.
FT REPEAT 1785 1796 REPEAT A.
FT REPEAT 1797 1808 REPEAT A.
FT REPEAT 1809 1820 REPEAT A.
FT REPEAT 1821 1832 REPEAT A.
FT REPEAT 1833 1844 REPEAT A.
FT REPEAT 1845 1856 REPEAT A.
FT REPEAT 1857 1867 REPEAT A.
FT REPEAT 1868 1879 REPEAT A.
FT REPEAT 1880 1891 REPEAT A.
FT REPEAT 1892 1902 REPEAT A.
FT REPEAT 1903 1914 REPEAT A.
FT REPEAT 1915 1926 REPEAT A.
FT REPEAT 1927 1938 REPEAT A.
FT REPEAT 1939 1950 REPEAT A.
FT DOMAIN 3536 3620 DEATH.
FT VARSPLIC 1039 1039
FT VARSPLIC 1444 3528
FT CONFLICT 475 476
FT CONFLICT 971 971
FT CONFLICT 3581 3582
FT CONFLICT 3586 3586
SQ SEQUENCE 3924 AA; 430337 MW; 52AC496C428E29D2 CRC64;
O -> OPLGKHLPTAPPPLNGESLVSRILQLGPPGTR
(IN ISOFORM 2).
MISSING (IN ISOFORM 2 AND ISOFORM 3).
GQ -> PE (IN REF. 4).
I -> S (IN REF. 1).
OY -> HA (IN REF. 1).
I -> Y (IN REF. 1).
Query Match Score 29; DB 1; Length 3924;
Best local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 QSRTEVL 8
Db 1336 RSRDVEVL 1343
RESULT 11
VC12_SPVKA STANDARD; PRT; 75 AA.
ID VC12_SPVKA P32221;
DT 01-OCT-1993 (rel. 27. Created)
DT 01-OCT-1993 (rel. 27, Last sequence update)
DT 01-NOV-1995 (rel. 32, Last annotation update)
DE Hypothetical protein C12.
GN C12L.
OS Swinepox virus (strain Kasza) (SPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirus.

CC NCBI_TaxID=10277;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=94069924; PubMed=8249275;
 CC Massung R.F., Jayarama V., Moyer R.W.;
 CC "DNA sequence analysis of conserved and unique regions of swinepox
 CC virus: identification of genetic elements supporting phenotypic
 CC observations including a novel G protein-coupled receptor
 CC homologue.";
 CC Virology 197;511-528(1993).
 CC -----
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 CC -----
 CC EMBL: L22013; AAC37859.1; -
 CC Hypothetical protein.
 CC KW SEQUENCE 75 AA; 9174 MW; 319A80660D64E9F4 CRC64;

Query Match 73.7%; Score 28; DB 1; Length 75;
 Best Local Similarity 83.3%; Pred. No. 9.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 RDEVEL 8
 111111
 Db 58 RDEVEL 63

RESULT 12
 PDXJ_SYNY3 STANDARD; PRT; 242 AA.
 AC P72776;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyridoxal phosphate biosynthetic protein pdxj.
 GN PDXJ OR SLR1779.
 OS Synecocystis sp. (Strain PCC 6803).
 CC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 CC NCBI_TaxID=1148;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=97061201; PubMed=8905231;
 CC Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 CC Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
 CC Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 CC Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
 CC Tabata S.;
 CC "Sequence analysis of the genome of the unicellular cyanobacterium
 CC Synecocystis sp. strain PCC6803. II. Sequence determination of the
 CC entire genome and assignment of potential protein-coding regions.";
 CC DNA Res. 3:109-136(1996).
 CC -----
 CC -1- FUNCTION: CATALYZES THE CONDENSATION OF 1-DEOXY-D-XYLULOSE-5-
 CC PHOSPHATE (DXP) AND 1-AMINO-3-OXO-4-(PHOSPHOHYDROXY)PROPAN-2-ONE
 CC TO FORM PYRIDOXINE 5'-PHOSPHATE (PNP) (BY SIMILARITY).
 CC -1- PATHWAY: DE NOVO SYNTHESIS OF PYRIDOXINE (VITAMIN B6) AND
 CC PYRIDOXAL PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE PDXJ FAMILY.
 CC -----
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 CC -----

DR EMBL: D90900; BAA16791.1; ALT_INIT.
 KW Pyridoxine biosynthesis; Complete proteome.
 SO SEQUENCE 242 AA; 26518 MW; 4F9E8FD215C3876E CRC64;

Query Match 73.7%; Score 28; DB 1; Length 242;
 Best Local Similarity 62.5%; Pred. No. 37;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QSRDEVEL 8
 111111
 Db 53 QSRDEVEL 60

RESULT 13
 Y456_MYCGE STANDARD; PRT; 334 AA.
 AC P47694; Q49238;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MG456.
 GN MG456.
 OS Mycoplasma genitalium.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 CC Mycoplasmataceae; Mycoplasma.
 CC NCBI_TaxID=2097;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=ATCC 33530 / G-37;
 CC MEDLINE=96026346; PubMed=7569993;
 CC Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 CC Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 CC Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
 CC Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lueker T.S.,
 CC Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 CC "The minimal gene complement of Mycoplasma genitalium.";
 CC Science 270:397-403(1995).
 CC [2]
 CC SEQUENCE OF 86-182 FROM N.A.
 CC STRAIN=ATCC 33530 / G-37;
 CC MEDLINE=94075230; PubMed=8253680;
 CC Peterson S.N., Hu P.-C., Bort K.F., Hutchison C.A. III;
 CC "A survey of the Mycoplasma genitalium genome by using random
 CC sequencing.";
 CC J. Bacteriol. 175:7918-7930(1993).
 CC -----

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 CC -----

DR EMBL: U39727; AAC72476.1; -
 DR EMBL: U39732; AAB01646.1; -
 DR EMBL: U01790; AAD10612.1; -
 DR TIGR: MG456; -
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 19 39 POTENTIAL.
 FT TRANSMEM 55 75 POTENTIAL.
 FT CONFLICT 181 181 F->S (IN REF. 2).
 SO SEQUENCE 334 AA; 38354 MW; D142C358CE474C71 CRC64;

Query Match 73.7%; Score 28; DB 1; Length 334;
 Best Local Similarity 75.0%; Pred. No. 54;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QSRDEVEL 8
 111111

DB 222 QNIDTEVL 229

RESULT 14
HA19_CANFA

ID HA19_CANFA STANDARD: PRT: 362 AA.

AC P18466;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE DLA class I histocompatibility antigen, A9/A9 alpha chain precursor.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-90316611; PubMed-2370086;

RA Sarmiento U.M., Storb R.;

RT "Nucleotide sequence of a dog class I cDNA clone,"

RL Immunogenetics 31:400-404(1990).

CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

CC THE IMMUNE SYSTEM.

CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

CC MICROGLOBULIN).

CC -----

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CC -----

DR EMBL: M3283; AAA30865.1; -.

DR PIR: A45845; A45845.

DR HSP: P30685; 1A98.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003597; Ig_c1.

DR InterPro: IPR001039; MHC_1.

DR Pfam: PF00047; Ig_1.

DR Pfam: PF00129; MHC_1; 1.

DR ProDom: PD000050; MHC_1; 1.

DR SMART: SM00407; Igcl; 1.

DR PROSITE: PS00290; Ig_MHC_1.

KW MHC I; Transmembrane; Glycoprotein; Signal.

CC FT SIGNAL 1 24 DLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

CC CHAIN 25 362 A9/A9 ALPHA CHAIN.

CC FT 25 362 A9/A9 ALPHA CHAIN.

CC FT 25 362 A9/A9 ALPHA CHAIN.

CC FT 25 362 A9/A9 ALPHA CHAIN.

CC FT 25 362 A9/A9 ALPHA CHAIN.

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CC FT 25 362 A9/A9 ALPHA CHAIN.

CC FT 25 362 A9/A9 ALPHA CHAIN.

CC FT 25 362 A9/A9 ALPHA CHAIN.

CC FT 25 362 A9/A9 ALPHA CHAIN.

AC P34767;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Ribulose biphosphate carboxylase large chain (EC 4.1.1.39) (Rubisco

DE large subunit) (Fragment).

DE RBCL.

OS Alisma plantago-aquatica (Damassonium).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Alismaceae; Alisma.

OX NCBI_TaxID=15000;

RN [1]

RP SEQUENCE FROM N.A.

RA Chase M.W., Solitis D.E., Olmstead R.G., Morgan D., Les D.H.,

RA Mishler B.D., Duvall M.R., Price R.A., Hills H.G., Qiu Y.L.,

RA Kron K.A., Rettig J.H., Conti E., Palmer J.D., Manhart J.R.,

RA Syste K.J., Michaels H.J., Kress W.J., Karol K.G., Clark W.D.,

RA Hedren M., Gaut B.S., Jansen R.K., Kim K.J., Wimpsee C.F., Smith J.F.,

RA Furler G.R., Strauss S.H., Xiang Q.-Y., Plunkett G.M., Solitis P.S.,

RA Swensen S., Williams S.E., Gadek P.A., Quinn C.J., Egulate L.E.,

RA Golenberg E., Leary G.H., Graham S.W., Barrett S.C.H., Dayanandan S.,

RA Albert V.A.;

RT "Phylogenetics of seed plants: an analysis of nucleotide sequences

RT from the plastid gene rbcL."

RL Ann. Mo. Bot. Gard. 80:528-580(1993).

CC -I- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF

CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC

CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF

CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH

CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME

CC ACTIVE SITE.

CC -I- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) -> 2 3-

CC phospho-D-glycerate.

CC -I- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) ->

CC 3-PHOSPHO-D-GYCERATE + 2-PHOSPHOGYCOLATE.

CC -I- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.

CC -I- SUBCELLULAR LOCATION: Chloroplast.

CC -I- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.

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CC -----

DR EMBL: L08759; AAA85294.1; -.

DR HSP: P00876; 4R0B.

DR Mendel: 2897; ALP1; rbcL.1.

DR InterPro: IPR000685; Rubisco_large.

DR Pfam: PF00016; Rubisco_large; 1.

DR Pfam: PF02788; Rubisco_large.N; 1.

DR PROSITE: PS00157; RUBISCO_LARGE; 1.

KW Photosynthesis; Carbon dioxide fixation; Photorespiration;

KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.

KW NON_TER 1 1

FT ACT_SITE 192 192 BINDING OF CO(2) ACTIVATES THE ENZYME.

FT NON_TER 394 394

FT SEQUENCE 394 AA; 43967 MW; 07C2DA05D1A322C2 CRC64;

SQ

Query Match 73.7%; Score 28; DB 1; Length 394;

Best Local Similarity 50.0%; Pred. No. 66;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSRDTEVL 8

DB 21 QTKRDTIL 28

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

ID RBL_ALIPL STANDARD: PRT: 394 AA.

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Job time: 214 sec

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